

50	55	60
Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp		
65	70	75
Met His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala		
85	90	95
Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly		
100	105	110
Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val		
115	120	125
Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala		
130	135	140

## (2) INFORMATION FOR SEQ ID NO:277:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Met His Ile Thr Leu Asn Ala Ile Leu Arg Ala Ile Phe Gly Ala Gly		
1	5	10
Gly Ser Glu Leu Asp Glu Leu Arg Arg Leu Ile Pro Pro Trp Val Thr		
20	25	30
Leu Gly Ser Arg Leu Ala Ala Leu Pro Lys Pro Lys Arg Asp Tyr Gly		
35	40	45
Arg Leu Ser Pro Trp Gly Arg Leu Ala Glu Trp Arg Arg Glu Tyr Asp		
50	55	60
Thr Val Ile Asp Glu Leu Ile Glu Ala Glu Arg Ala Asp Pro Asn Phe		
65	70	75
Ala Asp Arg Thr Asp Val Leu Ala Leu Met Leu Arg Ser Thr Tyr Asp		
85	90	95
Asp Gly Ser Ile Met Ser Arg Lys Asp Ile Gly Asp Glu Leu Leu Thr		
100	105	110
Leu Leu Ala Ala Gly His Glu Thr Thr Ala Ala Thr Trp Ala Gly Arg		
115	120	125
Ser Asn Gly Ser Thr Gly Thr Pro Thr Cys Ser Arg Leu Trp		
130	135	140

## (3) INFORMATION FOR SEQ ID NO:278:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1           5           10           15
Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
 20           25           30
Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
 35           40           45
Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
 50           55           60
Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
 65           70           75           80
Val His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
 85           90           95
Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
100           105           110
Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
115           120           125
Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala Arg Arg Ser Asp
130           135           140
Gly Lys Leu Val Leu Gly Ser Ala Asp Gly Ala Val Tyr Thr Leu Ala
145           150           155           160
Lys Asn Pro

```

## (i) INFORMATION FOR SEQ ID NO:279:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (iii) SEQUENCE DESCRIPTION: SEQ ID NO:279:

```

Trp Gly Ala Pro Pro Ser Gly Gly Pro Ser Pro Trp Ala Gln Thr Pro
 1           5           10           15
Arg Lys Thr Asn Pro Trp Pro Leu Val Ala Gly Ala Ala Ala Val Val
 20           25           30
Leu Val Leu Val Leu Gly Ala Ile Gly Ile Trp Ile Ala Ile Arg Pro
 35           40           45
Lys Pro Val Gln Pro Pro Gln Pro Val Ala Glu Glu Arg Leu Ser Ala
 50           55           60
Leu Leu Leu Asn Ser Ser Glu Val Asn Ala Val Met Gly Ser Ser Ser
 65           70           75           80
Met Gln Pro Gly Lys Pro Ile Thr Ser Met Asp Ser Ser Pro Val Thr
 85           90           95
Val Ser Leu Pro Asp Cys Gln Gly Ala Leu Tyr Thr Ser Gln Asp Pro
100           105           110
Val Tyr Ala Gly Thr Gly Tyr Thr Ala Ile Asn Gly Leu Ile Ser Ser
115           120           125
Glu Pro Gly Asp Asn Tyr Glu His Trp Val Asn Gln Ala Val Val Ala
130           135           140
Phe Pro Thr Ala Asp Lys Ala Arg Ala Phe Val Gln Thr Ser Ala Asp
145           150           155           160

```

```

Lys Trp Lys Asn Cys Ala Gly Lys Thr Val Thr Val Thr Asn Lys Ala
      165      170      175
Lys Thr Tyr Arg Trp Thr Phe Ala Asp Val Lys Gly Ser Pro Pro Thr
      180      185      190
Ile Thr Val Ile Asp Thr Gln Glu Gly Ala Glu Gly Trp Glu Cys Gln
      195      200      205
Arg Ala Met Ser Val Ala Asn Asn Val Val Val Asp Val Asn Ala Cys
      210      215      220
Gly Tyr Gln Ile Thr Asn Gln Ala Gly Gln Ile Ala Ala Lys Ile Cys
      225      230      235      240

```

## (2) INFORMATION FOR SEQ ID NO:280:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

```

Asp Val Val Glu Ala Ala Ile Ala Arg Ala Glu Ala Val Asn Pro Ala
 1          5          10          15
Leu Asn Ala Leu Ala Tyr
      20

```

## (2) INFORMATION FOR SEQ ID NO:281:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

```

Leu His Pro Ala Gly Ala Thr Asn Gly Ser Gly Gln Leu Ala Leu Pro
 1          5          10          15
Val Glu Ala Pro Pro Arg Ser Val Pro Ser His Gly Glu Pro Leu Gly
      20      25      30
Ser Ala Ala Pro Glu Gly Leu Glu Gly Glu Phe Asp Asp Arg Ile Asp
      35      40      45
Glu Arg Phe Pro Val Phe Ser Ser Ala Ser Leu Ala Glu Ala Leu Pro
      50      55      60
Gly Pro Leu Thr Pro Met Thr Leu Asp Val Gln Leu Ser Gly Leu Arg
      65      70      75      80
Ala Ala Gly Arg Ala Met Gly Arg Val Leu Ala Leu Gly Gly Val Val
      85      90      95
Ala Asp Glu Trp Glu Arg Arg Ala Ile Ala Val Phe Gly His Arg Pro
      100      105      110
Tyr Ile Gly Val Ser Ala Asn Ile Val Ala Ala Ala Gln Leu Pro Gly

```

```

      115              120              125
Trp Asp Ala Gln Ala Val Thr Arg Arg Ala Leu Gly Glu Gln Pro Gln
      130              135              140
Val Thr Gln Leu Leu Pro Phe Gly Arg Pro Gln Leu Ala Gly Gly Pro
      145              150              155              160
Leu Gly Ser Val Ala Lys Val Val Val Thr Ala Arg Ser Leu
      165              170

```

## (2) INFORMATION FOR SEQ ID NO:282:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: protein

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```

Val Gly Val Val Gly Val Gly Ala Thr Ser Pro Ala Gly Ala Gly Ala
 1              5              10              15
Gly Ala Gly Ser Ala Gly Thr Gly Ala Gly Ala Gly Gly Gly Ala Thr
      20              25              30
Lys Gly Arg Ile Asp Ser Ala Ser Ala Leu Ala Ala Pro Leu Ser Thr
      35              40              45
Gly Leu Leu Ala Val Pro Ser His Thr Thr Asn Gln Arg
      50              55              60

```

## (2) INFORMATION FOR SEQ ID NO:283:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: protein

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

Met Ala Asn Thr Gly Ser Leu Val Leu Leu Arg His Gly Glu Ser Asp
 1              5              10              15
Trp Asn Ala Leu Asn Leu Phe Thr Gly Trp Val Asp Val Gly Leu Thr
      20              25              30
Asp Lys Gly Gln Ala Glu Ala Val Arg Ser Gly Glu Leu Ile Ala Glu
      35              40              45
His Asp Leu Leu Pro Asp Val Leu Tyr Thr Ser Leu Leu Arg Arg Ala
      50              55              60
Ile Thr Thr Ala His Leu Ala Leu Asp Ser Ala Asp Arg Leu Trp Ile
      65              70              75              80
Pro Val Arg Arg Ser Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu
      85              90              95
Gln Gly Leu Asp Lys Ala Glu Thr Lys Ala Arg Tyr Gly Glu Glu Gln
      100              105              110

```

Phe Met Ala Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Pro Ile Glu  
 115 120 125  
 Arg Gly Ser Gln Phe  
 130

## (2) INFORMATION FOR SEQ ID NO:284:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Pro Gly Ser Phe Ala Arg Thr Lys Pro Pro Gly Arg Thr Ala Asp Ala  
 1 5 10 15  
 Pro Ile Arg Cys Arg Asp Ser Arg Gly Thr Ala Gly His Arg Ala Leu  
 20 25 30  
 Asp Glu Pro Pro Pro Arg Gly Ser Glu Pro Ala Arg Arg Arg Ser Arg  
 35 40 45  
 Gly Val Arg Thr Val Val His Asp Ser Leu Ala Ala Arg Arg Val  
 50 55 60

## (2) INFORMATION FOR SEQ ID NO:285:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Gly His Gly Gly Gln Ser Ala Ile Gly Leu Gly Gly Gly Ala Gly Gly  
 1 5 10 15  
 Asp Gly Gly Gln Gly Gly Ala Gly Arg Gly Leu Trp Gly Thr Gly Gly  
 20 25 30  
 Ala Gly Gly His Gly Gly Ala Arg Arg Trp Tyr Arg Gly Pro Thr Ala  
 35 40 45  
 Ala Arg Ser Gly Arg His Gly Arg Arg Gly Trp Arg Arg Trp Ala Asp  
 50 55 60  
 Arg Gln Arg Arg Gly Arg Arg Arg  
 65 70

## (2) INFORMATION FOR SEQ ID NO:286:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Asp His Arg Arg Arg Ser Leu Ala Ser Leu Arg Ser Ala Ser Ser Pro
 1           5           10           15
Ala Arg Ile Thr Glu Val Arg Pro Cys Thr Pro Leu Leu Glu Arg Ser
 20           25           30
Ala Pro Gln Ser Gly Ser Arg Asp Pro Phe Arg Pro Trp Pro Ala Asp
 35           40           45
Ala Gly His Ala Arg Ser Pro Ala Trp Tyr Arg Leu Gly Ala Gly Asn
 50           55           60
Pro Ile Pro Val Arg Ala Ala His His Glu
 65           70

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```

CCGCACGTAA CACCGTGAAT TGAAGGGAGC CGCTGGTCAT GGGCCGATTC TATCCGTGGG      60
CGACCGGTTA TTGACGGCCC GGAGGCTACT CGGCTGCCAC CAAGTGTGA CTCAGCGGCT      120
TTTCAGGGCA ACGAACGGCG GACACACAC TTGACATTGG ACAGCACGGC CCGG      174

```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```

TGCCTAAACGG GGTGACCTTC CGTCCGGTGG CGCTAGAGAG TTCTCTCCAC TTTCGGTGA      60
CGCTGCGCCG GCACCGCAGC ACCGGTGAGC TCACCTGCT ACTGGAGGTG CTCGACGGTG      120
CGCTGGGCAC GATGGCCGCC GAAAGCTTCG GCAGGCGGGT GCTGGCTGTG TTACAGCGCT      180
TGGTCAGCCG GTGGGATCGG CGGCTGCGCG ACCTCGACAT TCTGCTGGAC GCGGAGCAGG      240
ATCCGACCGC ACCCGCCCTG CGGATGTGA CGACGTCGGC ACCCGCGGTG CATACCGGCT      300
TCGCGGAAT CGCTGCGGCA CAGCTGACT CGGTGGCGGT CAGTTGGGCG GATGGTCAGC      360
TGACGTACCG GGAGCTGGAT GCATTGGCG ACCGGCTGGC CACT      404

```

(2) INFORMATION FOR SEQ ID NO:289:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

Ala Asn Gly Val Thr Phe Arg Pro Val Ala Leu Glu Ser Leu Ser His
 1           5           10           15
Phe Pro Val Thr Val Ala Ala His Arg Ser Thr Gly Glu Leu Thr Leu
 20           25           30
Leu Val Glu Val Leu Asp Gly Ala Leu Gly Thr Met Ala Pro Glu Ser
 35           40           45
Leu Gly Arg Arg Val Leu Ala Val Leu Gln Arg Leu Val Ser Arg Trp
 50           55           60
Asp Arg Pro Leu Arg Asp Val Asp Ile Leu Leu Asp Gly Glu His Asp
 65           70           75           80
Pro Thr Ala Pro Gly Leu Pro Asp Val Thr Thr Ser Ala Pro Ala Val
 85           90           95
His Thr Arg Phe Ala Glu Ile Ala Ala Ala Gln Pro Asp Ser Val Ala
100           105           110
Val Ser Trp Ala Asp Gly Gln Leu Thr Tyr Arg Glu Leu Asp Ala Leu
115           120           125
Ala Asp Arg Leu Ala Thr
130

```

## (2) INFORMATION FOR SEQ ID NO:290:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```

GCTTCGACGG CTACGAGTAC GTGTTCTGGG TGGTTTGTGC GGGCGCTTAC GACGACAAGG      50
CCAGAAGAC CACCAAGGCT GTGCGCGAGC TGTTCGCGGT CGCGGGGGTG AAATACTTGG      100
TGCTGGGGCG TGGGGAAGCT TGCAACGGCG ACTCGGCGCG CGCTTCGGGC AACGAGTTCC      150
TCTTCAGCA GCTGGGACAA CAGGCGCTCG AGACCTGCGA CGGTTTGTTC GAGGGTGTGG      200
AGACCGTCTG CGGCAAGATC GTTGTCACTT GCGGCGACTG CTTCAACACC ATCGGCAAGG      250
AATATCGGCA GCTGGGCGCC AACTACAGCG TGCTGCACCA CACCGAGCTG CTCGATCGGT      300
TGGTGCGCGA CAAGAGGCTG GTCCCTGTCA CTCGGGTTTC TCAGGACATC ACCTACCACG      350
ACCGTCTCTA GCTGGGTCGG CACAACAAGG TCTACGAGGC ACCACGGGAG CTGATCGGTC      400
CGCGGGGGGC CACCTEAGCC GAGATGCCGC GCGATGCCGA CCGCAG      450

```

## (2) INFORMATION FOR SEQ ID NO:291:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

- (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

CTCCGCGCCG	TGATCTGGCC	GCGGAAC TTC	GTCACTGCAT	CCAGACCCCA	ACGATCATCG	60
ATCAGGCCGA	TGCCCCATGAT	CACCCACCC	GCCACCAGCA	CCCGGGGCAT	GCCCGTGGAA	120
TAGACCAACC	CCCCGGTGAAG	TGCCCCGAAGC	TGGGAGCCAA	GAAAGACGGC	GCCGACCAATG	180
CCCAGGAACA	TGCCCCAACC	ACCCATCCCA	GGGGTAGGCC	TGACGTGCAC	ATCTCGCTCC	240
CGCGGTAGG	CGACCGCTCC	CAGCGACTG	GCCAGCATCC	GCACCGGACC	GCTCCCAAAA	300
TAGCTGATGA	TGCCCCCGGT	CAGCCCGACC	AGCCCAAGCT	CACCGAGCCG	GACACCGGCE	360
CGGCHATAGG	ACAGGCGGAG	CAAGCCACCG	GCAACCGCGG	CCACATCCCT	GGACACCTCC	420
AGACCGTACT	GCACCAACCT	GAGAGCTGA	ACACTCCCGG	AACGTGCAAC	AGGTCCGAAC	480
AATTGGG						487

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

ACGAAGCGCC	AGAATATGAG	CCGGGCAAC	CCGGCATGTA	CGAGCTTGAG	TTCCCGCGCC	60
CTCAGCTGTC	GTCTCCGAC	GCGCTGGTC	CGGTGTGGT	GCAGCTTTC	GAAGGTTTC	120
CGAGCGCGG	CCATCGGATC	CGCTGGCCG	CGGGCCACCT	CAAGCGCGCC	CTGGACACAG	180
AGCTGGTCGC	GTCTTTCGCG	ATCGATGAAC	TACTGGACTA	CCGTCCCGCG	CGGCCATTAA	240
TGACTTTCAA	GACCGATCAT	TTCACCACT	CGGATGATCC	TGAGCTAAGC	CTGTATGCGC	300
TGCGGACAG	CATCGGCACC	CCATTTCCTG	TGCTGGCGGG	TTTGAGGCGG	GACCTGAAGT	360
GGGAGCGGTT	CATCACCGCC	GTCCGATTCC	TGGCGAGCG	CTTGGGTGTA	CGGCAGAAC	420
ATCGGCTTGG	GCACCGTCCG	GATGCGGCTT	CCGCACACAC	GACCGATCAC	GATGACCGCT	480
CATTCCAAAC	ACCGGAGCT	ATCTCCGATT	TTCAGCCGTT	CGATCTCC		528

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

CCAAGCGCGT	CAAGGACCGG	GTGCGCGCTT	TGCTTCCGCT	GCCGCGGAGG	CCCGCGTTGC	60
CGCGGTTGCG	CGCGTTGCGG	CGGTAACCGG	GGTTTCTAC	GGTGGCGCGG	CGCGGACGCA	120
TGCGCGCGCT	GTTTAGGCGG	TTTTCGCGCG	CGCGCGCGTC	ACCGGCTTTC	CGCGCATGCG	180



```

CCCCCTTCCC GCGCTGGTG GGGGTGGCGG CTTGGTTGAC GTATTGTTCC ACCGCCCCCG 240
CCCTTGACCT TTTCGCGTG TCGATCGCGG CCGTATGGA TCGCCGACC ACGACCTGCG 300
AAGCCTCGCC TCGCGCGCA GCGGCCAAC TGTGTGCGG CTCTGCGAT TTGGCCCCCG 360
CCGACGAGAT GATGGGCACC ACCGAGCCT GCGGCGTCT GCGGAGGCG ACGCGCGTT 420
CGCGGTCAAG CCATACGCGA CGGTGCGCG CCGCTTCGA GATTTGACG CTGCGTTGCA 480
CCAGATCGAG CAGCGGTGTG CCGAGGACT GCGTACGCC GTTGGCGCG CCGTTGTAGC 540
GCGGAGCGCA ATATCGGTSC CCACTCGACC CAACCGCGAC TCCATAAGCG ACACCATTCG 600
CGGTGATGC
610

```

## (2) INFORMATION FOR SEQ ID NO:294:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

```

Phe Asp Gly Tyr Glu Tyr Leu Phe Trp Val Gly Cys Ala Gly Ala Tyr
1           5           10           15
Asp Asp Lys Ala Lys Lys Thr Thr Lys Ala Val Ala Glu Leu Phe Ala
20           25           30
Val Ala Gly Val Lys Tyr Leu Val Leu Gly Ala Gly Glu Thr Cys Asn
35           40           45
Gly Asp Ser Ala Arg Arg Ser Gly Asn Glu Phe Leu Phe Gln Gln Leu
50           55           60
Ala Gln Gln Ala Val Glu Thr Leu Asp Gly Leu Phe Glu Gly Val Glu
65           70           75           80
Thr Val Asp Arg Lys Ile Val Val Thr Cys Pro His Cys Phe Asn Thr
85           90           95
Ile Gly Lys Glu Tyr Arg Gln Leu Gly Ala Asn Tyr Thr Val Leu His
100          105          110
His Thr Gln Leu Leu Asn Arg Leu Val Arg Asp Lys Arg Leu Val Pro
115          120          125
Val Thr Pro Val Ser Gln Asp Ile Thr Tyr His Asp Pro Cys Tyr Leu
130          135          140
Gly Arg His Asn Lys Val Tyr Glu Ala Pro Arg Glu Leu Ile Gly Ala
145          150          155          160
Ala Gly Ala Thr

```

## (2) INFORMATION FOR SEQ ID NO:295:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

```

Arg Arg Arg Asp Leu Ala Gly Glu Leu Arg Gln Cys Ile Gln Thr Pro
 1           5           10           15
Thr Ile Ile Asp Gln Ala Asp Ala His Asp His Arg Thr Gly His Gln
 20           25           30
His Arg Gly His Ala Gly Gly Ile Asp Glu Pro Pro Gly Glu Cys Arg
 35           40           45
Lys Leu Gly Gly Lys Lys Asp Gly Ala Asp Asn Ala Gln Gln His Arg
 50           55           60
Gln Pro Thr His Pro Arg Gly Arg Arg Asp Val His Ile Ser Leu Pro
 65           70           75           80
Arg Val Gly Asp Gly Ser Gln Ala Thr Gly Gln His Pro His Arg Thr
 85           90           95
Gly Arg Lys Ile Gly Asp Asp Arg Arg Gly Gln Pro Asp Gln Arg Lys
100           105           110
Leu Thr Gln Arg Asp Thr Gly Ala Ala Ile Gly Gln Gly Glu Gln Ala
115           120           125
Thr Gly Asn Ala Gly His Ile Ala Gly His Leu Glu Thr Val Leu His
130           135           140
Gln Pro Glu Glu Leu Asn Thr Arg Arg Thr Cys Asn Ser Cys Glu Gln
145           150           155           160
Leu

```

## (2) INFORMATION FOR SEQ ID NO:296:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

```

Glu Ala Arg Glu Tyr Glu Pro Gly Glu Pro Gly Met Tyr Glu Leu Glu
 1           5           10           15
Phe Pro Ala Pro Gln Leu Ser Ser Ser Asp Gly Arg Gly Pro Val Leu
 20           25           30
Val His Ala Leu Glu Gly Phe Ser Asp Ala Gly His Ala Ile Arg Leu
 35           40           45
Ala Ala Ala His Leu Lys Ala Ala Leu Asp Thr Glu Leu Val Ala Ser
 50           55           60
Phe Ala Ile Asp Glu Leu Leu Asp Tyr Arg Ser Arg Arg Pro Leu Met
 65           70           75           80
Thr Phe Lys Thr Asp His Phe Thr His Ser Asp Asp Pro Glu Leu Ser
 85           90           95
Leu Tyr Ala Leu Arg Asp Ser Ile Gly Thr Pro Phe Leu Leu Leu Ala
100           105           110
Gly Leu Glu Pro Asp Leu Lys Trp Glu Arg Phe Ile Thr Ala Val Arg
115           120           125
Leu Leu Ala Glu Arg Leu Gly Val Arg Gln Asn His Arg Pro Gly His
130           135           140
Arg Pro Asp Gly Arg Ser Ala His Thr Thr Asp His Asp Asp Arg Ser

```

145		150		155		160								
Phe	Gln	Gln	Pro	Gly	Ala	Ile	Ser	Asp	Phe	Gln	Pro	Phe	Asp	Leu
		155		170		175								

## (3) INFORMATION FOR SEQ ID NO:397:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Lys	Pro	Val	Lys	Glu	Pro	Val	Pro	Ala	Leu	Pro	Pro	Val	Pro	Pro	Thr
1			5						10				15		
Pro	Ala	Leu	Pro	Pro	Leu	Pro	Pro	Leu	Pro	Pro	Val	Pro	Gly	Phe	Pro
		20						25				30			
Thr	Val	Pro	Pro	Pro	Gly	Ser	Met	Ala	Pro	Leu	Phe	Arg	Pro	Phe	Ser
	35					40					45				
Pro	Ala	Pro	Pro	Ser	Pro	Ala	Leu	Pro	Pro	Ser	Pro	Pro	Leu	Pro	Pro
	50					55				60					
Leu	Val	Gly	Val	Ala	Ala	Trp	Leu	Thr	Tyr	Cys	Ser	Thr	Gly	Pro	Ala
65				70					75					80	
Leu	Asp	Pro	Leu	Ala	Val	Ser	Ile	Ala	Ala	Ser	Met	Asp	Pro	Pro	Thr
		85						90					95		
Thr	Thr	Cys	Glu	Ala	Ser	Pro	Ala	Ala	Ala	Ala	Gln	Leu	Cys	Arg	
		100					105				110				
Gly	Ser	Cys	Asp	Leu	Ala	Pro	Ala	Asp	Glu	Met	Met	Gly	Thr	Thr	Gly
	115					120					125				
Ala	Cys	Gly	Arg	Leu	Gly	Gln	Ala	Ser	Ala	Gly	Ser	Arg	Ser	Arg	His
	130					135				140					
Thr	Arg	Arg	Cys	Ala	Ala	Ser	Gln	Ile	Cys	Arg	Leu	Arg	Cys	Thr	
145			150					155					160		
Arg	Ser	Ser	Ser	Gly	Val	Pro	Arg	Asp	Trp	Val	Ser	Pro	Leu	Ala	Pro
		165						170					175		

Pro Leu

## (3) INFORMATION FOR SEQ ID NO:398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

AATTCGGCAC	GACGAGCACC	AACACCGGCT	TCTTCACTC	CGGCGACCTC	AATACCGGTA	60
TGGGCAACAC	CGGCGACTTC	AACACCGGCA	GCTTCAATCC	GAGGATTC	AACACCGGGG	120

ATTTCAACCC	ANGCAGCTAC	CACACGGGGA	CTCGGAAACA	CCGGCGATTT	TACACCGGCS	180
CCTTCATCTC	CGGCAGCTAC	AGCAACGGGT	CTTGTGGAGT	GGAAATTATC	AGGGGTCATT	240
GGNTGCACTC	GGGCTTTCGA	ATCCCTCGKG	CCAATTCAAC	TCTTCNACAA	GCTTGCGGCC	300
GCACTCSAGC	CCGGGTGAAT	GATTCAGTTT	AACCGCTNAN	CAATAACTAG	CATAACCCCT	360
TKGGGCTCT	AAACGGGTCT	TGAAGGGTTT	TTTGTGAAA	GGANGAACTA	TATCCGGATA	420
ACTGGCGTAN	TACGAAAAGC	CGCAGCGATC	GCCTTCCCAA	CAGTTGCGCA	CCXGAATGGC	480
AATGGACCC	CCTKTTACCG	GSCATTAAAC	CGGGGGTGTN	GGKGTACCC	CCACGTNACC	540
GCTACCTTCC	CANNSSCTTN	RSGCCGTCTT	TCSTTTCTTC	CTTCCTTCTC	CCMCCTTCC	600
GGTTCCCTTC	AGCTCTAAAT	CGGGGNNCCC	TTTGGGTTTC	CAATTATTGC	TTACNGSCCC	660
CCACCCCAAA	AAATNATTTG	GGTTAATGTC	CCTTMTTGGG	CNTCCCGCTA	WTNANNTTTT	720
TCCCCCTTNA	CTTTGRTTCC	CTTCTTTATN	NTGAMNCTNT	TTCCACYGGA	AAAMNCTTGA	780
CCNTTYSSES	TTTCTTTTGA	WTTATMRGGR	AATTSCAATY	CCGCTTTCGG	TTMAANTTAA	840
CYATTTTCTA	ATTTTCCCGM	TTTMMNATR	TTNSNCKCGM	KNTCCNKA	SSGNTTTCCT	900
CCCCCTTSS	GKTYCCCGRN	G				921

## (2) INFORMATION FOR SEQ ID NO:299:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

AATTGCGCNC	GAGATANGGG	CGACCCGGGG	TCCGCAGCCG	CGGGGACCGT	CGCCAGCACC	60
ACCGGGGTCA	ACAGCACCCAC	GCTGGCGTCC	ANGCAGAGCG	CCGCGGTGAT	GGCGGCCBAG	120
ACGGCRAACA	CCTGCCGTAG	CAGTCGGTGC	GACTCCGGCC	TGGCTCGANC	CATCGCCGCG	180
CGCGCTGCTT	CGAACANGCC	TTGCTCGTCC	ACAGCTTAGC	CAGCANCCAA	ACCGCACCCA	240
GAAACODACA	CGCCCGCCGC	CCCGGANACC	TGCGCCATCG	KCTGCTGGGG	CGANATCCCC	300
CGATCCCTNA	CANGATGACC	GCTGCCGGAA	CGCCCGCCCT	GCTTCGGGCG	AGCCGCTTGG	360
CGCGGGCAAC	CGGGAACCCA	NGAACACGGC	AAGCAGTATC	ANCGCAACAG	CAATTGTCTA	420
GGGCTAAACG	CTTCACATCC	AGGATCTTCG	CGCCGCCACA	CCGTCCGMTC	TGCAGSOGGA	480
CCCTNTGCTN	GGCGGNCAC	TCTTCAAAGA	TGCGGATCNA	CAGKCTAGGT	CTTCGGCCGA	540
TATGSAAGGN	CGCAACGGNT	TTAAAGCGGC	GAAAAAATC	TCCANTOGA	TAAAATCGGC	600
CGGGGANCCC	CCCTGSCMM	NGTGYCGGKC	ATTNTTCAAC	MGCTTTNACG	CGGKTGCGC	660
GCCAACTKCC	CAAMTTAAG	KTNGGGGNTY	CGGGGCGSTA	ACCGGCTNTX	NGCCCTTAA	720
AAAACCGGNC	YTTCTKGAT	TAMMCTCGN	CCCCCANTGG	CGGKTGKTCC	CAGNTTYAAC	780
AMCCYCCGCS	MNGGCKTGG	HAACCTTCC	CGNGGGGTTT	NTKGTTCCT	AWMCCCCCGG	840
AAACCGGKYG	GGKTGGCTN	WASSAMNCCC	CMNGYTTCTT	TAAAGGCCAN	KHRAAWOKYT	900
CCTTGGGAAN	CTTCAATYC	GAAAAYCTC	CTYMMGSSCN	CTTKCWRTYN	NRNGGGAACS	960
AMWTNYGCMC	GWTTCAWTCC	GGTCCGASMN	AAACKETTTY	TTTTYCGSSC	STCCMGGSNC	1020
GGTTGNANAN	AAASATTTMC	YVCNNNANKX	YYCSCGCTT	CYKNGRNNR	GMCAACCCGR	1080
GS						1082

## (2) INFORMATION FOR SEQ ID NO:300:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

AATTGGCAAG	AGTATGAGG	CTGAAGCCCG	TAGCCGCGGT	GGCTCGGGTG	GTTCGGGAAC	60
RAAATCCGCT	CGAGTGGTC	TGGTAGGCG	GTGTCCANAA	CGGTGGCCCG	GTGCGGCGCG	120
ATCTGATCCG	CGCGGCCGA	GTGCACCTCG	CGCGGCGTGT	GCASTCCGAT	GCCCGAATGC	180
TTGTGTTGCT	GGTTGTACCA	GCCGAAGAAC	CGGTGCGAGT	GCACCGGGGC	CGCTTOSATC	240
GACTCGAACC	GTTCGGGAA	ATCGGGCCCG	TACTTGAAGG	TCTYGAACAG	GGCTTCAGAC	300
AACGGGTTGT	CTTGTCTGTC	TGCGGGCGTG	AGTCCGACTT	GCTGACACCG	AAGTCGGCCA	360
NCANCAATGC	CACCGGTTTG	GAACTCATCC	ACAACCCCGG	TCCGCGTCMA	GGTCACTTGT	420
NCGCGCTTAA	TTTNTGCGC	GGCAAGGTTT	TGCGGAYCAN	KCCGCTCGGC	CAAAACTTCG	480
ANTCNCSCCA	AGGCGGCCAT	CNCGCCAACC	AMGTTACGGG	ANAAANATY	CAGAGAYCAC	540
CYTCCGGTIN	TTATANGTYC	CCYTTTGSTY	GGCGCCCGCN	CYYTGKKNAT	AGCCCTNCCA	600
AWTCCCAACN	CCCKCCANA	RCYEGGGGCG	CCNCCCAACC	CGGGKGAAGA	WTAATTTAAA	660
CCCYAACMAN	ACTWMMNACC	CNNGGGGCGY	AAMCGTYVNR	AGGTTTTTCT	NAAAGRAASA	720
ANTCGGAAMC	CGGNTSTACC	AAAAASCCK	CCNWTCCCTC	CRASATTGSC	NCCSAAWKSA	780
AKGCCCCCHY	TGCGGNWNNC	CSGCGGKXKT	KGGTNSCCT	WMRCNMWYTS	GGCCNASCCN	840
CKYYSMYCC	CCCTTCCCM	CTCGGNKTPC	CCAMCCYAMC	MOGCCCCCHM	GKCCCCWKNY	900
YKCCCCCCCC	AMNNNNCGGG	WGAACCTTNG	CCCGMKRSGM	TCCCNANTGA	MOCTCNGHRA	960
MKCYCCNRAE	ANMCCSCNCC	NGCNCRCXON				990

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

AATTGGGCTG	GCAACSCCGG	CTGTTCGSCC	AACCGCGGCG	CGGTGCTTCC	CGGTGGGGCT	60
GGTGGTGGCG	CGCGCGGCGC	GGCGGTAAC	GCGGGGTGCT	TGCTTCATCG	GGCGCTTGGC	120
GGCTGGGCTG	GTGTANGTCC	GGCGGGGCGC	AACGCTGCTA	CGCGCGGTCA	GGATGGGGCG	180
GCTGTGTTTG	CGGGGTCCGA	CRACCTCTCT	GCGCTGCTTG	CCG		223

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

AATTGGGCAC	GAGCGGCGAA	CGGTGGCAGC	GGCGGCACCT	CNCTTCCAC	CGGGGGGGCG	60
GGGAACGGCG	GTGCGGGTGG	CGCGGCGGCG	GGCGGCGGCG	TGATCGGCAA	CGGCGGCAAC	120
GGCGGCGGTC	GGGAATGGCG	CGATGCGGCG	GGCGGCACCG	GGCTCNGCGG	CATCGTGGCG	180
CTGTGTGTTG	GTTCGACRG	CGGCAACGCG	CGGCGGAGCA	CCAACCGGCT	GCACACCGCG	240

CAGGCAAGGC	GTTGGCCGCA	GTCAAGGCGC	CCATCCAGGC	CTTGACCGGG	GGCCCCGAT	300
CGGCAACGCG	CCAACGGGCG	CCCCGGCAAC	GGGGCCCCCG	GCGGCAAGCG	CGGGTGGTTG	360
TTGGGGGGCG	GAAGGAACCG	CGGGTCCGCG	GTCAACGCGC	GGGCGGGCGG	AAATGCGG	420

## (2) INFORMATION FOR SEQ ID NO:303:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

AATTCGGCAC	GAGGGGCGCG	ATCCGATACA	GGGGTCCGCG	CAGACCCGCG	CGATACGCGA	60
GCTCGGCGCA	CGCGAGCGCG	CAATACGGCG	TCTGGGTGTC	CGGCTTGAGC	ACGACCCGCT	120
TACCGGGCAC	CAGCGCGCGC	ACCGAGTCCG	ACACCGTAAG	CGTCAATGGG	TAGTTCCAGC	180
GGGAGATCAC	CGCGACCGCG	CCCTTCGGTT	GATAGCAGAC	CGTGGTCTTG	CCATACCGCG	240
GCAGCAGCGG	CTGTGCGTTA	CGGGGCTTCA	GCAGSTCCAC	ACAGACTCGT	GCSTTATAAT	300
TGCGGCTTCC	GCGATCAGAT	CGACAATTTC	CTCTTGCGCG	GGCCATCGCG	CCTTCGCGCG	360
CTCGGCTTCC	AGGAAAGTCC	TGAAGAACTC	GGGGTTCTCG	ATNAACAGGT	CGCGATAGCG	420
GCAGATGACT	GCAGTGGCT	CGATNACGGG	ACCTTCGCGA	GTGCGTCTCG	CGCGCGCGAG	480
CTTCGCGCGA	TGCGGCTTCC	ACTTCGCGCG	NCGTGCGCAC	GGATCTATAT	CACGGGTTGC	540
CGGTTAAAG	TCTCAATST	NCYGGTGGAA	ATTGCGCGAC	TTCTTATGCC	GGCAGGTRCC	600
AACGANNCAA	ACCTCGCGAA	GCTTAGGTTT	TCCCGGCTTT	YCAAAAATNC	GGGTTTTGNN	660
CMAATTTGCG	CKGNATGKTG	MCAAGGTTCT	CKAANAAGCG	GGGTCTCTCN	NTGNGKGGAK	720
CCAAAGGGGT	TGGGGGAGCG	GKNMNCAGAN	CCTWAGGCTG	KTKAAGGNNW	TTCCCCCGCG	780
GGGAKKNGGA	ATTCYCCGNA	NCGCGGGGGG	GNNCAGATTC	TYCGGGMCTC	CTCKGGAWTC	840
WONGSTTTTC	CAAAAAACGC	CCCAATTTM	TTTTTCNNCN	TTTGGANACN	CTTTTKARCA	900
MMGSSAARNS	ANMNCCTCYC	CKCTNTGKTK	AAAAAGNAYW	CCCGMAAATT	TYTAWTTGSC	960
CGCGCGCGGN	CGGCTCTGTT	TGCTNTWCTM	WNYTNCNMCC	MMMSNCKSNG	KGGGNCCTNN	1020
CGCGGCGCGN	AAWYNTXGYN	KNTATMAGC				1049

## (2) INFORMATION FOR SEQ ID NO:304:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

AATTCGGCAC	GAGGGAATCG	AGAATCCGCG	AATGGTGAAG	CGTGGGTGCG	TGCGGTTACG	60
CCAAGAKTCA	GGTTGAGCGG	CCCCCGGCGT	GGAATGCTGA	GGCGAAGCGG	GAAAAGCGTG	120
AGGGCTGGGG	TGGAATAACT	GAAGTTTACT	GGGATGGAAG	ACCGGATATT	GATATGTATT	180
GGGGCGATCA	AGTTTGTGGG	AATGGGGGAA	GGCTGAGGGC	GACCTGTTTG	ATTTGGCGAA	240
TTGTATGCGA	CGAGACGCGC	CAGCGGCGGT	GATGGTTTGG	TTSAANYTTT	GTGCGGCGCA	300
CAGGTGATG	GGATTGATTT	TGATGCGGCG	GATGGAATA	TTGGGTATGC	CGACCGCGAA	360
CGAGATYCG	GGGACGTTCA	TGGGCGGGAC	AACCGAGGTT	CCGAGGTAAG	GGTTTCTCTN	420
ATTTGATCG	GGATTGCGCA	ACTMTGTGGA	TGGGCTGCAV	MTSATGCGCG	NACNCGCGCG	480

YTTATTTCMS	GCTNAYGGGA	ATRAMGGAA	CAAYNTCCCT	CCCMGGAAAA	ACCAACMSGC	540
CTTGSTNSYC	CNCCCRCCNC	AKAACCCRTT	KCTGTSTMC	CCSMAAATNA	CSCCCCCTTS	600
NACTCCNC9G	AANTNSCCCC	CCCSCHNNTT	ATSTYCCCGK	STTCCCCCMC	CCCTTNAAMC	660
TCCCCGGTTA	ACCCCCWNTT	SNCCNCCCGS	YTAAMNCRG	GCTTSTTNGT	CCCCCYTRMX	720
CNCCCCCTCK	SAMCWNCCNC	CTCXAAACNAC	CCCKCYKQSM	TNCCCAATNT	WCMWCKCCHS	780
KTNTMTCTKC	CCAAITNCRC	CCNCRCTCCG	CKKSTSTCAM	WTATAAAACC	WCMYANYNNE	840
KCNWMAWTA	MGACNCTCNV	NCCCCNCCCK	NTTSTAMWCC	CKMCCCKCSW	TWCYCKCSCC	900
CCNTCTNNAC	YCCCCCKKTY	NKWMCCCTTC	CCSCCCTCCG	MCNMBHKTCT	YCSGKTWCMC	960
NCNTTMTCTN	CYNANMCKCK	KTCTCTTCCH	CKSTCTCCCG	CCWCCSCCTV	KKCTCTSKCC	1020
CNCTCTCCSC	MMKSCC					1036

## (2) INFORMATION FOR SEQ ID NO:305:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:305:

AATTCGGCAC	GAGATCATGA	ATAGCCGGCT	GCTCAGCACC	GAAGTGGTGG	GCGATCTCGC	60
GAGCAAGTCT	CGTCTGCTCG	CCGACGAGGA	GGTCGGCATC	GATCGCGACA	CCTCGCATGT	120
CTTGGAATGGT	GTTCACTTGC	AGSTAAGGCC	GACGCGCGAG	CTTTGCTAGC	AGGCTGTCTT	180
GGCTCTTCCG	ACGTGAGGTA	ACCAATAACT	CCGACGCGAG	CCAACTCCGG	CCCTCGATCC	240
GGGTACGAGG	CTCGCGCGGA	GCCAGCCTTT	GTCCSCCTTG	GGCCGAAGGT	CAGCTGCTGT	300
GCGATCGAAG	TAAGAAACCG	CGCATGCCCC	GTGCGCAAGT	ACGACTGACC	GAGCAAAACGA	360
ACGATCGTGG	TGCTTTCGCT	GGGGGTATTC	GAGCCGAGCA	ACCGCAGGAG	CCACCAATCA	420
TTGGGATTCG	GCCACTGACC	GACCAACCGC	CTGTGCGACA	CCCCAGCGGA	ATTGGTGGTG	480
TTCCCGCGGG	CCGMAACCGG	AATLANCGGG	ACCGCTCCGC	CGAASCANCC	GCATANCCNT	540
ACATANCAAC	GGNTCTCGCG	CCGACATTTC	GGGTTMTTCC	CCCTTNGCAA	CSNAAYNCC	600
CCCAATTCYG	AACMAAALAA	TTGGYCCATY	ARNGTYCTCM	CCMAAAACCN	AWTCCCCKTA	660
TCCCCCGGGG	GGGCCCCCTY	NMMAALACCG	CCWMAAMCC	CCSGGGGSCC	CGGGTTRWTH	720
CCCCCTGTCT	GGCCNCCSGG	TTTGGTCMCM	GGSCMWTNWN	GGNTGCGCC	CCCNCTRAAA	780
AAAAAYCKNG	NCAATYAAA	CCCKYMAAAA	ASKTGGGGSC	CCMAACCGCG	GGKAAKKNWA	840
ANTTAANCXY	KAAAAAAAWK	NCAANMCCCC	NGGCMCCTAA	GGKYTTAGCG	GTTGTTNANG	900
AAAAAATMTC	CAATMNSK	TTNNAAAAAA	ASCCSWAKCC	CCNNINKKNN	CCAAWKAARR	960
SRCTTCCGGG	TMWNSGGGGG	KXKXKTNCMS	KMMMTTWGR	CCNCCGCCCN	NNTWKECTTN	1020
TCCNYGGNGC	RNCAGN					1036

## (2) INFORMATION FOR SEQ ID NO:306:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:306:

AATTCGGCAC	GAGTGCATTC	GATCGAACAC	GGCGGCACCT	GGCGAGGCCA	CATGGCGCGG	60
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GGCATGGGCEA	ACGGCTACTC	GGCCACCCCG	AATCCATTTC	GCCTCTCACC	GCAACCCCGG	120
AAACCGGGGGA	CGCGGGGATG	GATCAACCCG	CCCACCCCG	ATCCGAAATA	GCCTCCACAT	180
AATGAGACAC	TGGCGCAAAG	AGCTTGACAG	GCGCGGACCC	ACGCAAGCTG	TTAGACGTGT	240
CGGTCTTGCA	AGAAGGGGGT	TGGCCACCCA	AGATCACGCC	GCCCCAGGGC	ATCGACTERA	300
CGTTGCGGTG	CTACCGCGCT	AACGTGCGCG	CGCCCAAGAA	ATGACGGTGC	GCAATACCAT	360
GGCCCTGCTG	ATCAGCTTTC	GGCACCTGCG	CACCAAAACT	ATGANCAGCC	TTATGCCGAG	420
TCTCGTGGAC	ATCGGCAGCC	GCTTCAAAAA	CTCCTTGTCG	ACAATSGTAT	TGCTGANCCTG	480
CCGAATTCCT	NTGCTTGCAA	SAACACTNCA	TGTTNCGGT	NAACAACCTT	GCTTNGAAAA	540
ACANCCATA	TTGAANTCCC	ANTCGGCGAM	GAACCGTTM	CGGAAGTGGK	TGGGAACGAA	600
TGKTGCCCCA	AAATCCCCCG	NGGTRAAAWW	CCCNENATGG	MSAATTTTSC	CTNGAACRAM	660
AAAAGGTCCA	AGKYCAAAGG	NGCCCCCCCC	SONAAATTGG	TGAACSCAKA	WYANRTTCCC	720
WWNTNCRAAT	MTNGGGSTCC	KNNTCCCCWT	AAANGGSCN	CCCCNCCRG	GMSTTTCCCC	780
NWNMGGMGN	CYYCSCCCCA	AAAAAAAMMM	MTTTCGSGG	SMGGKKCCCC	CCSGGTWGG	840
GKNTTTAAAC	CGGKGGGYN	CAAAAAAMAN	ACCCCECAMS	NGGGGGGAAA	ATTTNGAANT	900
AAGGKKTTC	SCMACCCCAA	AAANMMNCH	AMNCCCGMK	SARGGGGNY	TTMKAGGGMG	960
GNYCCCCCN	YCGGGGGGNA	NAAYAAAAGK	NSNGRGGAAT	NTTNTTTTCK	RSSSRNKTIT	1020
TYNTCCTYCN	CCRMGNRWNG	SRAMNTGHTS	NSSGGGSCCC			1080

## (2) INFORMATION FOR SEQ ID NO:307:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

AATTCGGCAC	GAGCTTCACC	AAAGAGCTGA	CATGCGGGGT	GATGCGACAT	CGCATCGAGG	60
GCAATACCGG	CATGGATGAN	CCBAANGGAN	TCTGGCTTC	GCTCAACTGG	ATTACGGTTC	120
CCAAGGTGAA	ACGCTTTTGG	GCAAAAGATG	CGACGCTTAA	CTTGGCGTTT	CACCTTGCAA	180
TGTTGATATG	GATGCTGAAA	CGCGCTGAC	NGATAANGAA	TTGCTGTGTC	GCGGGGCACN	240
ATGGAATGTC	CKSTTTTENC	TCCSCGTTA	AATTGCTGT	GCATCATCTG	GCAGGCTATG	300
TTCCCGCTAC	CTGCGAGCCC	ATCATGGAIG	TCCGGCTAAC	GAANAAGTTA	TGACATGGCG	360
CAAGCGAMTC	GGGCATGNC	CGCGCANTTT	CGCAACCTGC	TGTGINTGAA	GCTMTCAAC	420
CGAATGCGGG	GCTYAAAAGC	NGGCTTGGCT	TGATTMMAAC	CNAACCCCTN	CNATYCTTTC	480
CGGNGMGTG	CGTCTCTTCC	AACTCGSKG	SYTGCCNCCG	TGAAACCCNA	CTNCCCCCCC	540
GTTGGACTTA	MRTNTTCAA	AAMCGEMTNA	ACCGAATINN	SAACCTNCCG	TCAAANTAMM	600
SAANTCGGGC	TTYGGENRCC	CCCCNGAAYN	TTCKNCNGGG	GMRNTYCTCN	GCTTYNGGCG	660
SAAACTTTTT	GCTNCGYMN	TTACAMGGC	NMTNMTTGM	GCGSCENNAS	GWCCCCGGKX	720
TNTTNCANW	TGNCNKTIT	TTGGGGGGGG	GGCYORTFMC	NGGGGCCCCC	GGCCCKMAA	780
AAAAAMCMA	RRCCNCTYGG	KCCCCCCCCM	NNATNGGGCG	YKRAAACAA	ACCCCAANEA	840
TNONGMGGGC	SMACCCGNGN	GYNAAAKGCT	TNSCTMANM	MKGMANNNCT	SGMSCMNSN	900
NCTGMGGGKT	TTKGNWGAAN	AANAMKMGCM	RCGGNCSCNN	GAAAGCGSMS	GSCKECNNGN	960
NGASNGWGMN	CRNNGANRCC	NCNGYGMNRN	NNGNNNGNWN	GGGRKNACN	NMKMCANSMC	1020
NENMGNNNN	CGYWTNKGCC					1080

## (2) INFORMATION FOR SEQ ID NO:308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

AATTCGGCAC	GAGACAANGG	CCTEAAATGG	GATCCGCCCC	AGCTGGGGCC	GGTCGTGAGC	60
CACCTGTTCG	CCAACTGCGG	GCCGCGGTTT	CCGGTCTATG	GGCCCTAGTT	ATCTGCGCCG	120
AGCGTGAAGT	CAGGGCGAGA	TTTCGGCCGT	TTTCTCGCCC	TGGCTTCACG	TTCCGCGAAG	180
TKGGGAACCG	TCAGCGTTCC	CAAACACGSA	TCGGGATCGT	CCGGTGGGTC	CAGGACTGGT	240
ANTCCTGATA	CTTGGGTACA	TCGTGACCAA	CTGTGNCNAA	TATTCGGGCG	GCTCCTGCTC	300
NGTCGGGTCG	CGCGCGGTAA	GGTCCANCA	TTCTTTTTTC	TCGTGCGG		360

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

AATTCGGCAC	GAGAGACCGG	GTCTTGACCC	AACGGAGCGT	TGGGCGCGGG	CCCTTTGCGT	60
GGCATCAGCC	CTTCTCTTTC	TTAGCGCCGT	AACGGCTGCG	TGCTTTTTCG	CGTTCTTGA	120
CACCTTGCGT	ATCCACCGAA	CCGCGGATGA	TCTGTAGCG	CACACCGAGC	AGGTCTTCA	180
CCGGGCGCGC	GGCACCAGCC	ACCATCGAGT	GTCTCTGCGG	GTCTGCGCCC	TGGCGCGGAA	240
TGTAAGCGGT	GACCTCGAAC	TGACTCGTCA	CTTCACCGCG	GCAACCTTCC	GAAGCGCGCA	300
GTTCGGGTCG	TTTGGAGTGG	TGGCTCTGCG	CG			332

(3) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 962 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

AATTCGGCAC	RAGTCGGTCT	AGACGGATTC	AATGCTCCCG	CGAGCACCTC	GGCACTGCAC	60
ACCGTGCAGC	AAAATGTGCT	CAATGTGCTG	AACGAGCCCT	TCCAGACGCT	CACCGGCGCG	120
CCGCTGATCG	GCAACGCGCG	CAACGGGACT	CCTGGAACCG	GGGCTGACCG	GGGGCGCGCG	180
GCTGGCTGTT	CGGCAACGCG	GGCAACGGCG	GGTCCGCGCG	GAACGGAACC	AACGGCGGGG	240
ACGTGGGGAC	GGGCGCGCGG	GGATTCTTTC	GGACCGCGCG	ACCGGCGGGG	CGGGCGGGCT	300
CGCACACCGG	CACCGGCGCG	GACCGCGCGG	CCGTGGGGCG	GCTTCTGAGT	GGGCTCGGGC	360
GCTNACCGGG	CACGGCGCGG	CCCGGCTCAC	CGCGTGTTCG	GACCGGGGGA	CGCGTNACCG	420
CGATCTTCTT	CGCGNCGCGG	GAAACCGCGG	GGCGCGCGCG	ACATTAKACC	CGCGCGNACC	480
CGCGNCGCGG	CGGAACCGGG	GGYNTTCTTC	AACGGCGCGG	CGCGGGAACC	GNMGGCTGTT	540
GCTTNGGGGA	AGGNCRAKT	CCCGKCTANC	VYAATCGCGG	ANGGKTGAMC	CTSATGNCNA	600
MYTTMAGGAA	CYTNCCCAAT	XTTSCNACCN	CRGNGGAAA	ASRAWNKNOT	KGGCAAAACNA	660

NNTTCCTTTN	NATTTCGGNNA	AAAANCCCTT	CCWCSSRACT	NCCCCCNCNM	GGGMCNNTNN	720
NTTTYGNCN	CCCGGSNAAM	RNTTKATTC	NGGGGGNTCN	GGGTGMNNNA	AACCCCAAAM	780
MNNNNACSCA	ANGSSKSGC	NKNNMMNSGT	TTTTCKMRA	MNNWTYKNN	NTCNGARSRN	840
NAAMCNSNK	NGKKKNNKAA	AENNTTWKTN	KNSCHNCCMN	GRNGVVRGGC	CKMEGSENNK	900
MCWENAWRNG	MNGSNCNCKC	NNKNNAAAAA	AASGVNCKS	NEMKNYKKEG	NKGGGGGGGG	960
GG						962

## (2) INFORMATION FOR SEQ ID NO:311:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

AATTCGGGAC	RAGAAGACGC	CCGAANGTTT	GGCTGCGCTC	TACAACCTCA	TCAARCCCA	60
GGGGGAAGCC	AATTCGGCA	AGATCTACGT	TGCTTCCCC	GAAGCGGTCT	CGATGCCCA	120
GTACCTCGGC	GCACCGCAGC	GGCAGCTGAC	CCAGGATCCG	GCCCGGAAAC	GGTTTCGCTT	180
GCAGAAGATG	TCGTTCCAGG	TGGCTTGGAG	GATTTTGCAN	GCGACGCCNG	TGACCGCGAC	240
GGTTTTCGTG	TCCGCACTGC	TGCTCACCAG	CCGCGGCACC	GCCTTGACCT	CGACCCAGCTG	300
CACCACTGCT	GCCGCTCGTG	CCG				323

## (2) INFORMATION FOR SEQ ID NO:312:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

AATTCGCACT	GTGTGTGCGC	GCCTCCAGAA	GAAGATGATC	GCGAACATCG	CCACCCCGCG	60
CCAGGCTATG	GTGCGGTGA	TGGCCGACCA	GCCGATCATC	ACCGGCATAC	AGCCGCGCGC	120
CCACCCCGAC	ACCAGCTTCT	GTGACGTGCG	TGCTTTGAGC	CAGAGCGTGT	AGACRAACAC	180
ATAAAAGCGC	ACGGTGACCA	GGGCCAGCAC	CCCCGCCAGC	AGCTTCGTGG	CCACCCATAG	240
CCAGAAGAAC	GAGATCACCG	TGNACCTCAC	CCGAGTCCCA	ACCGCTTTCC	GCTCGGCACC	300
GCTTCCCGCG	CCAAGGCGCG	GCGCGCGCTT	CGCTTCATCA	CCCTGTGCGAT	ATCGGCGCTCG	360
GCAACCACTT	GAGCTGTCTG	GCGCGCGCGC	CAGCCATCAT	CCCGCCGACN	AGCTTCTTGA	420
GCATGANCAG	CGGATGAATG	GCGCGCGCGC	TGCTGCGGCT	CGTGCGGAAT	TCACTCCGCT	480
CHACAACCTG	CGGCGCACT	CGAACCCCGG	TGAATGANTG	AATTTAAACC	GSTSAACANT	540
AACTACATAA	CCCTTGCGGG	CTCTTAACCG	GTYYTGAANG	GCTTTTTTTC	TTAAAGGAAG	600
AACATTTTCC	GGATGCTGCG	CTTTNWTARC	GAAAAGGCCC	CRCCCATNGC	CCTCCACAGT	660
TTSCCGCTGA	ATGCGAATGG	MNCCNCCYKNR	CNGGGNCTTT	AACRCGCGCG	GGNTTTTTGKT	720
MCCCNCTKA	CNTTMMCTGC	ARNCCNCGCC	SKCCCTTCCK	TNTYCCCTCC	NTCCCCCNST	780
TNCGKCTCC	CNNAMPYTNW	ACGGGGGCGC	YINGCGKCRM	TWTKTTTGG	CCCCCNCCTC	840
MMAANASAA	GGGCKNGTY	CTTTTGGCNC	CCGAMAARCG	NYCCCCCNCN	YTNREKMCST	900
CNTTNGGNN	CTGTNCNCC	GAARLAMACC	KCCCCGNTS	STTNGTYWAG	GFRWKGNERS	960
CTCCCCCGGY	MNDNAAYAWN	MMNATNCNNS	STNANMAKEN	NNNNNNNSCN	MNENENNTCN	1020

SCNENGGKBC C5CC

1034

## (2) INFORMATION FOR SEQ ID NO:313:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

AATTGGGCAC	GAGCCGACAT	CCCGGGCCCG	TCGTTGCATG	ACTCGTTCCG	CATCGTCAC	60
RAGGCACAGT	CGCTGGAGCG	CAATGTGTTG	CTGACCGTGC	TGTCGCGGTT	GGGGACCGGT	120
TCCCGGCTGG	TGTTGACCCA	CGACATCGCC	CAGCCCGACA	ACCTGCGGGT	CGGCGGCGAC	180
GACCGGTCGC	CGCGTGATC	GAGAAGCTCA	AAGGTCATCC	GTGTTTCCGC	CACATCACCT	240
TGCTGCGCAG	TGAGCGCTCG	CGATCGCGCG	CGCTGGTCAC	GAGATGCTCG	ANGAGATCAC	300
CGGCGGCGCG	TGAGTGCGCC	TCCCGCGAGC	A			331

## (2) INFORMATION FOR SEQ ID NO:314:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

AATTGGGCAC	GAGATCGTCA	CCCTGGCGAC	CAGTGACCGC	AGGCCACGCT	ACCAGTTACG	60
GCTGATGGGC	CAGAAGATCG	ACCAGGTGCT	GGCCATCCCG	CCCACCGCAC	TGCAGCTGAG	120
CACCGGATCG	GGGTGCTCA	GCTACGGCGA	TRAGCTGGTG	TTCGGCATCA	CCGCTGACTA	180
TGACCGCGCG	TCCGAAATGC	AGCAGCTGGT	CAACGGTATC	GAAGTGGGTG	TGGCGGCTCT	240
GGTGGCGGCT	AGCGACAATT	CGTGCTGCT	GTTTACAAGG	ATCGGCGTAA	GCCTTCATCG	300
CGCGCACTCG	CGGCGCGCGC	CGGCGCGCGC	CGGCGCTCTG	TGCGGACCGC	CCGAGCGGCT	360
CAGTGACCGC	ATGTCGCTCG	GCGTTAAGCC	CGTGAGAGCG	TGGTCTGTCG	GCAAGTTGGG	420
CCCGGTCAGC	ATGATCCCGC	GCGCGCATGA	CGGCTGCTG	TTCACACCA	CNTENGACNC	480
CCCGGAGGAA	CTGTCGCGCG	AMTNCAGGAA	NTYCGTGTGG	GCACGCGCTT	CTTCGCTRT	540
GGCTTAAGCT	TGCTATTTT	CGCGCGGCTT	CTGGCGCTTC	CGCGCGGCGC	NTCTTNCCLAA	600
ATCGGCGGAA	ATCGCGGCGC	AAACCGCGCG	GGTCTTGGGG	GCAGCGGCGC	GGCGGAGGCG	660
AAACCGCGCG	NTTAAANTCT	TTGKTGCGCG	CNCGCGGCGC	NCNAAGCGCG	CGCTTTTGGCG	720
NTTGGCGCGC	CCCAWTTTAA	CCGAKCGGCG	AAACCGCGCG	TTMGCGGCTT	NTAAAGGAGAA	780
AATTTGGCGC	CCCAANTAA	ATTCCGCGCG	CCYTTGGCGG	CGRANCYNTT	TTTMCSSNS	840
TGCGGAGGAA	NGGAGCGCGG	KAAYTMMTGG	NAAYCGCGCG	AAMNTTTTTC	TAANNCGCGC	900
YNCCCGGAGG	ATTNAGGAA	CMNKTGCGCG	GGGKTTTENC	SGKKGAGCGG	AAAAAANREN	960
SKTTMCGGCG	SAMNCGGCGC	SGGNSNCGCG	NNNCGGCGCG	CSNAANMCGC	CGCGGCGGCG	1020
CGGCGGCG						1026

## (2) INFORMATION FOR SEQ ID NO:315:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

AATTCGGGAC	GAGAAGACGC	CGARNGTST	GGCTGGGCTC	TACAACTTCA	TCAAGCCGCA	60
NGGGGAACGC	AACCTGGGCA	AGATCTACCT	TCGCTTCCCC	GAAGCGGTCT	CGATGCGCCA	120
GTACCTCGGC	GCACCGCACC	GGAGCTGAC	CCAGGATCCG	GGCGGAAAC	GGCTTGCTTT	180
GCAGAAGATG	TCCTTCGAGG	TGGCTTGGAN	GATTTTGCAN	GGGACGCCNG	TNACCCCGAC	240
GGGTTTGGTG	TCCGCACTGC	TGCTCACCAC	CCGCGGCACC	GCCTTGACGC	TGACCAGCT	300
GCACCACTCG	TGGCGTCTCT	GCTT				324

(2) INFORMATION FOR SEQ ID NO:316:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1010 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AATTCGGGAC	GAGGCGTSCC	GSTNAACACC	AGCCCCCGGC	TGCGAGATAT	CCCGGACTCG	60
GTAGTCCGSC	CGGTGGCCTC	GTTCCTTCTC	TCACCGGCGC	CGGCGACCAT	AAGGTCCCTM	120
ATGCCCCAGT	AGCGGCCCCG	GTGCATGGAG	TCGATGATGA	TGCGACTCTC	CAGCTCGCCC	180
ACCGGGAGCT	TGGCATCGGG	CCTGATCAGC	CAGGACGCTT	AGGACAAGTC	GATCGAATCC	240
ATAGTGGCCT	CCAGAGTGGC	CCTGCAMTTC	CNGGCTGCTC	CACCGCAAAT	GCCTTGATTT	300
CTACTCGGCG	TANTTCTTCC	GCATCGCTTG	CGCGATGAAT	GGGAACCGCA	SGATGGCGAC	360
GAACGGGTCT	GANTCAGCT	TGCGGCTTTT	GGCGACAGTG	GTGACACACC	GGTACTCGGC	420
ATANATCTGG	CCCNAAATCG	GGCGCGACCG	CGCCGACAT	AANAACGGGC	ACNACAATCG	480
CGCGCGCGCT	CACCNAAACA	ACANCTTGGC	ATCGGATTTT	GTCCCCANCG	CTCAAGCCCT	540
CGCGAAGGCC	TGNTCGGGCG	NACTTTTCTT	NNANTAAGTG	CGGCTTCCGK	CGCTGGGCGA	600
WTAAATGGGA	AACCGTNNCC	CCACCTTGAA	GGGCTTGCTT	NATTTTACT	GCTAACCCCC	660
AATNTTCCG	GANTCGGTEN	KCGGGGTTTT	YSTNTTCCCC	ACCTTNGNAN	GGGCGCGCCA	720
AGSITTTCTT	SYTGAAGGGG	GAAACCCAAC	TTTNTTYTYN	AACCCGNNAA	MYMTTTCYCG	780
MNAASCCNKT	CCCTTTTAAC	CAMGGGGGTN	AAACGKTMNG	NGGKTAAAAA	GGGSGNNKTC	840
NGCCCYMANG	GGGGGAAAAA	TSTKTGNNCG	GGGCGKAAAN	ACCMMMMYGN	GTGKKGNNES	900
GCSAAATTTT	NMMRAACTYN	GGGGCGSSGA	NNTTTNAAAG	MSCCCCCENN	GSTGKCCENN	960
NTTTCNNAA	NMKKGKNNNM	SNMNSCGNCG	GTNNSGGNNN	NNAAGGGGGG		1010

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1010 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AATTCGGCAC	GAGCGCTGCC	GCTNAACACC	AGCCCGCGGC	TGCCAGATAT	CCCGGACTCG	60
GTAGTGGCCG	CGGTGGCGTC	GTTCCTCTCC	TGACGGGGCG	CGCGGACCAT	AAGGTGGCTM	120
ATGCCCAGGT	AGCGGGCCAG	GTGCATGGAG	TGATGATGA	TGGGACTCTC	CAGCTGGCCG	180
ACCGGGAGCT	TGGCATCGGU	CTTGATCAGC	CAGGACGCT	AGGACAAGTC	GATCGAATGC	240
ATAGTGGCCT	CCAGAGTGGC	CTTGCAMTTC	CNGCTGCTC	CACGGCAAAT	GCCTTGAATT	300
CTACTCCGCG	TAMTGTTCGG	GCATCGGCTG	CGGGATGAAT	GGGAACCGCA	GGATGGCGAC	360
GAACGGGTCT	GANTCTAGGT	TTGCGGCTTT	CGCGACAGTG	GTGNACANCC	GGTACTCGGC	420
ATANATCTGG	CCCNAAATCG	GCGCGGACGG	CGCCGACNAT	AANAACCGGC	ACNACATCG	480
CCGCCCCGGT	CACCCNAACA	ACANCTTGGC	ATCGGATTTT	GTCCCCANCG	CTCAANCGGT	540
CCCGAACGGC	TGNTCCGCGG	NACTTTTCTT	NNAWTAAGTG	CGGCTTCCGK	CCCTGGNCGA	600
WTAAATGGGA	AACCTTTNCC	CCACCTTGAA	GGGCTTGTGG	NATTTTACT	GATAACCGCC	660
AATTNTTCCG	GANTCGGTCN	KCCGGGCTTT	YSTNTTCCCC	ACCTTNGNAN	GGCGCGGCCA	720
AGTTTTTCTT	SYTGAAGGGG	GAAACCCGAC	TTNTTTTYTN	AACCSOMNAA	NYMTTTYCSG	780
MNAASCGNXT	CCCCTTTAAC	CAMCGSGGTN	AACCGTMMNG	NGGKTAAAAA	GGGSKNNKTC	840
NCCCCYMAAG	GGGGGAAAAA	TSTKTCNNCG	GGGCKAAJAN	ACCHMMMYGN	GTGKXKXKSS	900
CCRAAATTTT	NMMRAACTKN	GGGGCCSSGA	NTTTTMAAAG	MECCCCCENN	GSTGKCCCMN	960
NTTTCNNMAA	WMKXGKNWNM	SNMNSCENG	GKYNSSGSEN	NNAAGMGGGG		1010

## (2) INFORMATION FOR SEQ ID NO:318:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:318:

NGNGGGGWN	NTCAYCAYCA	YCACSGGGY	EWATTGCGGC	CCCAWCTTGT	MAASAGATCT	60
CSAAYTCGGC	AMGAGGGANT	CKCTMGCCNC	GCTGTGCAAN	CCAATRAGGC	CTRATAATTT	120
CGACTCCACA	AAAAACCGTT	GTGTGTAYTT	SCCGRAAATR	AAGGCGCCCG	TNTCAACWYC	180
GGCGGTCTTY	CCATYVCCCG	TKTTGTAMCT	CCCKGGGTSR	AAAYCCCCCG	TGTTGGAYCC	240
CCGGAATTGA	ACTGCCGGKT	TGAAACTGCC	GKTTTSGGCA	TCCCGKWATT	GAMSTCRCCG	300
ATTAATAAAC	CGGKTTTGGN	GCTGNCCTG	CCAAATNCGR	AYCCRATAYC	CCATGGGCTG	360
KYCTVCTCCX	YCGGTACCCA	AAAYCTGGST	TGCTATACTG	GYCCCTAAAK	GCAAWYCKGG	420
GCTGYCMTX	TTGCKGGSGT	CCNAATTTAS	CACGACGGGT	TGCTTCLATA	CCNAAACNCG	480
CKTGGGCGCC	AGMCCGAAAA	AAAKAATAAT	EAKAAGGCTG	CATNYCCAAA	ACGNCGGCCN	540
CCCNANTNEN	ATCCGNTNCC	MSCNCCGCCA	GGGNTAAGK	TKSGGAAYTT	CTMMAACCCC	600
CAAAACCCCA	TACNTNCGR	GAASAAACCC	CTYCNCCGGG	GYCNWNCAAA	ACASCTTTAT	660
TTGCTKSTTT	CGCGMWCCGT	GCAGCCNAAA	YCCCAAATA	CTTTTGTGGT	CCNAGAKAAA	720
ACGNCGGGCH	CCMCCCSNAA	NWTATYTCTT	KGGCAANCCC	CSAAACCTTR	TCMNAACNCK	780
ATRMTCCTTT	CGCCVSCAAT	TGGYCGGRAT	NGGNCCTTY	TCAAAXKXSC	CAJONWNGNG	840
GRRIMACOMA	ACCCCAAGTY	CCMNAAAAATN	GKCCCCGCTC	CNAACACGNK	TYTCCSAAA	900
ASCCGCCCCC	CCGCCCCRAA	AAACCCCCNA	SKANTNCCCA	AAAACNYNGK	CGCCCCCCCC	960
CAAAACMAAAA	AMCCCCCGM	EMACSGGGGN	NMCCCCCKEK	KNTTTTCTTT	TKCCMRSCCC	1020
AAMGCAMWSE	KSKTNMAAAA	GGAAGRANCN	TYCCSANANM	TCCCNWRSW	CCGSGWNGNA	1080
GAASMCCCCC	CS					1092

## (3) INFORMATION FOR SEQ ID NO:319:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```

GGGGGGGNNNN NATAACATCWT CYGTGYACCG GGGMTCTAKT GGGGGGGGGG AATCTNGTCA      60
ASAGATCTCTT NANTTCGGGC ACRAAAACTW GACAAASVMT CNGGCMHTCC GTGTCTNKA      120
TCGCAAAACG NSTRACASAC ASACACRTAT GTGTGCGCAC CASCRAATTC TTGGGACCTC      180
GCTRACCGGY TGGGCMNAGE CCACGYTGCS CWTCTATCCC RAGCGCGGGC ACGGGYGGGG      240
ATATTGCAAG CACCAAGCGG AGTTTGCTGG ACAATGCGCT GGCATYTTCC TCRANNTTC      300
TGAAACCGAA TTCNEMTTGA ACCNCCAAAG CCCCNCCHNR AACARTTGGG WTCCGCGGTT      360
GTGCGGACCG KTTTCGGGGG GTNTGCGCAN AANCGCACCC WTGGWTTCTM TGNCCGACCC      420
GGGCGGACAA NTGCGGTTGC AATTTTGCGA AYCGGGGGCG GGATTCCGCA AACGGGTGCC      480
GAACTCTTTC YCRAAMACCG GGAACCGCAA TTTCGGGSCR ANAAATTTCT YCNACCCACT      540
GCTTTRACTT CCGCGACCTT AACMANTTTC ATCTCTNTW CCTCTGCGCT TGGGCGAGGG      600
CKAAAYACCG CMTTKGGTTT CUGAACCTGC GGGCCCAANTC CCNANCCRCA CTTCNATTT      660
GGNTCGAATT SCCCCCGGTT RANAAGCGCC NTGCGCCHVT CGGASSAAAA NGGCGCTNT      720
KGGCNCGGCC AGTAANACCG TACCHNATTS CMTCTTTGC CAAASTTGGG ACGAANSKTC      780
GGNTTCGGGK ATTTYTTTGS GGNCGCGCTN TATNGGNTN GGGGCKCYNC NCSTKTCGCA      840
NASSKAYCCS NGNKGGGGGT ACCCGCTTMO GGGGGTTTTT NSSCGCGCGC ANAYNKSTG      900
GGCGCCNNGG GGAANKATWT MWTMCHNSGG GGGAAWTTT NTSTEGAMES SGGACYCCCR      960
GGGGGTTTTT TCGCGNCBA NNANANGCGG GGGGGAAYT NTGNSGNGCG KMTTTTATT      1020
YTTYCYCCTM TKACMSGGGG GTTTKKAIDG GGGGGAGAAA ANAAAAAAA RAKGGYKFT      1080
TSENCACNCT GKNNNNWANE NAGAGKTCT CKKXCNCBG SNTTTCITTT MGNSSGYGG      1140
GNGNNAAAA ACNKSEMMAC KCTYTVCGGG CBYCTGCTCC NCGGGGGYGS NGSCGNSTYN      1200
GNNKGRKWTG TTNMGCGCTN SCCTCGNCCC GCKNKNTGTC TMTCHMYGSG C      1251

```

## (i) INFORMATION FOR SEQ ID NO:320:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```

AAYTCGGCAC MGAATATCAC CAACTGTYGT GGGCCAGCBA AGTGGAGCTA TTAATACCTG      60
TATGTGATCC TCRACATCTY CTCCCGCTAC KTGGTCTGGT GGATGCTGGC CTGCGKTGAK      120
TCRAAGGTCT TGGGCHAAACG GTTGATCGCG CAAGCCCTTG CCGCCAGCAC ATCAKCGCGG      180
AACAGCTGAC CTGCGCGGCG ACCGGGGGGY GNCATAACT CCAAGCGGT GGCMTGCTG      240
CTGGCGNACY CGGTGTCCCA ANTGGAACTC ASCCGCMA CCAKMAACKA NAACCGTTGT      300
CTGAAGCTCA GTTCAAAAAC CTCAGTNC CCGCCACTT CCGGAAACGG TNGAGTCKA      360
TCHSAGSGG CCGGTTCMC TCGAACCGGT TCTTCGGNTG GTRCAGCTT AAAMCAAGCA      420
TTCCGGGMYC CGMTTCCTA CCGCGCCAA TTMCTACGG GCGGSCCNAT CAAATTCGCG      480
GGGAACSGN CGNCKTCNK GGMACCGCC TNCRAAACG CYGHAACGGK ATCTTTCKGY      540
NAACNCGGA RCNCGCKSKT TCGGGCTTC NMSGCGAATA CCGKNSCHMT CGGAATCCAA      600
TTCCMKYGG CTTTTYYYCC TCGGGCGCC AAAYNCGGYC CTTASSNMKC KNCAMKANT      660

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CCNATCTCTG	NGGTCCCNAN	KYYGGCGTTC	NMAATEAMNA	NMNRGGGTYT	TSCYACCMNN	720
AACCGGKNG	KCCCGMECTK	MAAAAKATT	RATCAMYMG	GGNKKKCNCH	NAAMACCSCN	780
CNCYNWYTC	IMYSSKMG	GCSMYNANCA	SNEGGGAGGW	GGSGRMKCT	CTMTCTCNCY	840
MGCGCCXNTN	TYCKSGAKAT	ACASMKRTCC	CCCGCGCGCN	MAAMANRAKA	CTAKCCGYGN	900
CCSNSTMTYN	CTSNMMEMMN	TCCMMWATC	NTYVGEKCNW	KCTMKATNWC	CCCTSKCNCK	960
MEAMTCTTYG	SNMTCTCTCA	TONTCTCKSC	SNMSKNTCKC	KSCNCCNCWN	CNCKNMKCNW	1020
GGNSTCROCY	ICTMNNNTCS	AGCKCGSKNC	WACNCACACK	NGWCTYTTCC	WGNMKCNKM	1080
TKCKCACRO	MTMTQWCCS					1099

## (2) INFORMATION FOR SEQ ID NO:321:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GNONTATACA	TCWCTGTGYA	CCSAGGATCW	ANTGCGGCGG	MAAKCTWSTM	CASAGATCTC	60
AAAYTCTGCA	MGAGCGGCAC	AGAKYSTCGT	CCMNACCCCG	CAYACNCCWG	CNCGCCCCWT	120
CTTRGACCGG	GGCKATASMC	ACCGTTGSCC	CCGCGNCCCA	CCTACACCAC	CCACGCGGCC	180
AGCGCGCCCN	TRAMCAAACC	ACCGCCCKTT	TACCGCGCGC	GGCGCGCGGG	CCACCACCAG	240
CCCCACCGGC	ACCACCGGCG	CCCGCTTTC	CAAAACAGGC	CCGCKTTTTC	CACCRA	296

## (2) INFORMATION FOR SEQ ID NO:322:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:322:

NGNGSGNMY	ATCATCWTC	TGCACCSNGG	MTOWATTGCG	GGCGCAATCT	TSTMMASAGA	60
TCTCGAAYTC	GGCAGARCA	TCTGCGCGGN	GAATGTCCAA	AWGTCKTAA	CGGCMATCGG	120
TTTGCCGYCA	ACCACKCTBT	SCAKATGCGG	GCCAMWYCA	AACCRATTAT	TTGGGYCGAG	180
AAAATTTMCG	CKTGTRASCA	ACCTGCAGCG	GCTCAASCAA	CAGCCTCTRA	ACCGTAATY	240
CKTAGGTNKT	YCGGSCAACA	ASCYCRATAA	TSCGCGCGCG	AMCCACAAA	CCTGANTNGT	300
TNTTCNCRAA	NCGGGTGCC	GRAGGGTGA	ACTGCSGTAR	GCTTNTCNYC	NCCTTRACAT	360
TAAACCCCCC	CGGNTCWTCC	CGCGCCCCAA	ATYCYTGCCC	WTGSCNACCA	YCCCANCCCTG	420
CGGTATGGTE	RAANCASTG	GCRAACGSTM	MCCSTACCKC	TGGCTGATYC	KTCGNTCCS	480
SHAATTGCGG	GAITTTACGG	CAMGTTTAA	CCAGGYCCCC	TFTGCTCKY	CNACACCCSG	540
ATCMWNCOCG	TACCTNTTAA	AATTCTTGT	GCTGGAACCC	AWYCKAAAA	NMENTYCCCN	600
TCCAMMGGGG	CYCGGAAXKT	CNACNTGGKT	NACCCCTNCC	YTTGAASTTT	TCYTGNCCTCC	660
GGCCCKAAAS	ANACCGGAKC	CGCGGAAYCS	WTAGGCTYCN	TGCCCCSTTA	AATTGNCYCY	720
AATCKKCCAA	CGGTCCCCCG	GGTSSCCNT	TAAAMTTCCC	CCCKSCASNG	GAATYCYKSS	780
CGWGTMAATW	CCNCCNTTT	CYYGKAAAC	SCCCCCWEGN	GGCTYCCCN	SNTTSSGCCC	840
GOTTSGAMYC	AAAANTNGGG	MMCNBAGNCG	SGNAMCCSCN	GKGGGGSATW	TKAAYYCYGG	900
GGGGGTENYC	CCCCRCNAA	AAGYGTGCG	GGCGSSCCYC	CCMARTTTTYT	CNGGMRCHAM	960

ACCANGGGNG	CTCCCGTNCW	WGGCTCCCN	SNSMAMAAAN	NKCKCCNGGS	CKGAERPMNA	1020
MCTCSNNGGG	WTCCCKWKTC	NSCNSGNCGS	YDENSASWCC	YNYCNCCACA	ANC	1073

## (2) INFORMATION FOR SEQ ID NO:323:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

CGCCCCGGTC	TTMMMTTCAY	TCATTACCG	GGMTCTAGTC	CGCCCCCAAK	CTTGTTCACA	60
GATCTCGAAY	TGGGCAMGAS	ACAAATSTCGG	GTGCGSCAAT	GTGCGGTGGG	GCAACTTTGG	120
GCTCGGRAAT	YCGGGGTAA	CGCGGGGTCT	ATCGGTSTG	GCTAATATCG	GGTTTGTAA	180
TGCGCGCAGC	TACAAATTCG	GTTCGGCAAA	ATATGGGTGT	GGGCAATATN	GGGTTCGCTA	240
ACACCGSCAS	TGGAAATTTC	GATATTGGGT	NACCGGTAV	AAVCTGACCG	GGTNCGGTGG	300
TTTCAATACG	GCTAACGGGA	ATGTSGGTTS	YYYACGCCG	GGAACGGNWW	YTTNGKTCTT	360
TMMCNCTESH	CKSAAMTSM	KMGSTSTYCT	MTYCNMGAS	TANTYMMCCC	CCGWAYCKSC	420
WAYCCCTCGT	CATYCCMCMC	SGSGYCTCA	MNCCACCTG	NGYYCCCTCC	MMMTCTCAAT	480
CMSTCCGGTW	CCTNTMMGCC	CSCNCHYCTC	AMCNCTESGX	CACCNATMYC	CSACKCHTCT	540
MCYMCSCAKN	MTTCCCGCTN	CCTYTNDCCA	MCNCSCTCTM	TCHAACTCKC	CCGGYCKCNC	600
MYCTCTCKCC	AYDMAACCKX	TYCVNCHWYC	YMYCKCKCAG	WYXNMTCTCW	ACTCTMYNTE	660
TCTCTCNKCC	CMKACCGTTC	CTCNCSCCGC	CCACAKAYMC	YAWGNTWTCG	MCTCKACSCC	720
CVYCHNYCCM	MMCNMTCCWC	TWNAKCANCN	TTCTTCTCTC	MMYMTMACCK	WNNNTCNCKK	780
SGACCTCTCT	ACTCKKCKCM	TCTCTTCKCK	CCYMWCHTCC	MYNCCCTCTC	NMTCTCKCTT	840
CCTCNCHMY	CVYYAKCAKC	NMTCTCCCAN	KMCAKCTKCT	CCGCCAEMKS	ACNCKCCCCWC	900
CTTCTATATC	ACTCTCHCTY	ATCTCKCTCN	CNYCHMYMCK	ACNCKCHYAT	CNACTMNMWN	960
CCANCHCTCT	CTNYCTCHCK	ACTYCKCKCH	CTMCKCHWYC	NHWCTYRCCT	CKKCCNCCCN	1020
CCNMCHCKTN	CTCTCHNMKN	YCTYCCCAT	CTMKCTCTCT	WCHCHTCCCT	CKKCTYNYNT	1080
KCTYCCMYG	CTTCKCHTCT	WCHCHCATC	TCTMKCTCTT	CWCACYMCAQ	WMTTACWNCC	1140
ACTCTCTCHW	CKCKCKMCKR	MTCTCB				1166

## (2) INFORMATION FOR SEQ ID NO:324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

NNGGNNNNNT	CWTACATCWN	TCTNCACCGG	NGMTCHWATTC	CGCGCCGCAW	NCTTGTMMNAS	60
AGAAATCTCHN	AAATCGGAC	ANAGTCTCTT	TSTMTAKTGT	GGCGGGGNGC	CACGCKTAT	120
GTGCGCTTGG	GYTRACCCAA	CGCGCGCGCS	CGCGCTRACC	AGCGGGGGA	TSCAGGCGCG	180
GGCGCGCGCG	GCGGYTATAT	RAAGCGCGGY	TTTTYKTRATA	ACGCTSCCGC	CGCGGGGTRA	240
TTACCGGCAA	AAVCGGKTT	TTGGGTRTAT	AACGCTAATT	GCAACCAWTT	TTTYCGGCTC	300
AAAAACVCGG	CGWGCANATC	NCGGYCNCCT	RAGCGGCATT	YMGCCAAAA	WTNTGGGCGC	360
AAAACCCCKT	TSYTATTTTN	TGGGTATATC	GGYTCTCTTC	GCAACGCTY	CCCGGGTTAA	420



TCCCTCCGCG	GGGGGGGGGG	AAAAACCACC	AATYCCGYTG	GGGGTGKYYC	CMCAGGCGGT	480
TGCTTCGNGY	CACCTGGGCA	AAYVCCCAWT	AKATTGGGTS	SCYCKTSCGG	TTSYTGGGGY	540
CAATTACCCC	CNCGGCGNAA	GRRAAAANAA	ATCCTCCNTT	TGCTCGGYCA	YCTTTMTTGG	600
SAAAAGGGGC	ATGGGCGGCT	TYTTFACCT	CAAYCCGMA	NCANTWACCT	YCCSCCGCGG	660
GGGNCANAA	CGSTTNGCTC	CGSSGNAECC	TKGTMCCTCG	ATCNAAAGGC	CNGAATTTCG	720
TYYSSTYCN	ATTWTWGGY	CCDCWCTTTG	VAAAAAKCCA	AAASAKCCCK	YCNCAMMYKT	780
NGGGGTYSYG	GCKKTYCTK	SNWTTAAACC	CYCCCCAAAA	YVNSGGGKKT	TCCGCTNEAT	840
KCCACGCGCK	GNCGGCGGNA	SAAAAAAAY	TTYCCSAAA	ATCCGACCTY	TCYKTKSTRY	900
AMACCCCTTT	TYMKKAYTC	CKYSCNATTC	SGMTTCWAAA	TYCCGYGGCT	TNTTCCCGCK	960
CSGGNGCCCC	AAWTTTGKTT	YNCHANTTYC	CCCNAAAMNM	ANTWGGGKKS	KCCATTCTGG	1020
SCYTMAANTA	AAANAAGGG	NKTTTYCTY	MANAAACACN	GTGKCNENCN	CNRAAAAASN	1080
AKMAAAKAGN	KKNTKXNSA	AANCCNCCCC	CTSTYTNWTT	NKTNMNCCKC	CYGGKKNKGM	1140
SWSWYNTTCT	NCCCGCCCCC	YNYNCTGANA	RAMMNCYCCS	GGSTMCRNAN	ASNMTTTCCK	1200
STSTNGMGCC	KMBASHANAN	MCAMWKWYCC				1230

## (2) INFORMATION FOR SEQ ID NO:325:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

NGNGGGGKINA	TMAFCWTCTC	ACSSGGTCTA	TGCGGGCGCAW	CTMGYMAASA	GATCTCNAAY	60
TCGGCANNAN	GCATMTGMMC	CATATATAAC	CATTGCGTCS	GYWTGCAWCT	CHAANCTGTC	120
CTTCGKCCCC	TTTACRAAG	GTCGHWTOYT	CWTYCCTRAA	SCCCTCRATC	TCKTETATYC	180
CTKGGGCTYC	ACTTTAACSG	SATKSCCTCC	TTKTAYCATT	SATGCAANTB	WTGGYCRANT	240
XTTGCAGSGC	SAGGCGWYCT	TTYCCGCGRA	GRACAAENGA	TTGGAWYCCG	TYCCCRAGSC	300
CCGGCAGCTAR	ACCGGCGNCC	AAAGGYCCCG	CCAAWTSCTT	GGKTCAAAAA	TGGTGCLAAC	360
AAAMCHATCC	CGGGYTTTAC	CGCAGYTAMC	ACAARKAAAT	TCCGWTGGCC	GCACCAWNTT	420
TYCRATOWY	CWYCCCCACC	TTTAACTTCK	YTGGSTIATF	GCCTKCCCTCC	CTCRACAGCM	480
YCNCCCTICA	AACCTCGGCT	GACTCCAACT	GGTCTGGYCG	AASGGGGGYT	CAMCGGACAA	540
AACCCCRANN	TGSCCAAATT	TTGNCNCCCC	CYCGGGAAAN	GKTGATMTTC	TCNNAACCSA	600
CMGGGNNYTW	NAACCCGTGA	CSSSGSNKGA	MYNSCDSGGA	ANTTTTCCCT	TYNGGGGGRN	660
AAANCCTTTT	AAGGTACCCG	KCGNCGGGKG	CCCVYTTGGG	AAAACAACCC	CKATTGGKTT	720
TGGAAATNTT	TKCNCCCCCA	TTGNSGGGGG	GGGCCCCAMC	CCMCTTTTTN	TCMSCHNTYY	780
YCYVGGGAAT	TNYTCCCCCG	GAAYVCGGSM	CCKGYCCTAA	NCCCCNNWGG	GKYSTGSHAR	840
GGRAITMANWT	TYSTTTTYMC	CCGCGCNCCC	CCCKASMCNT	KONTGAACMA	AAAKCSGGGG	900
GGCNMYMWYY	YCNNGNNTT	TNRGSSNMT	TYMAAAMMAN	GGGGKYWTTY	CKCCNGSCNN	960
GKTYSGGGST	TTCCNTTTT	GGSSSATYKG	MACCCCKTWT	AYCCSGGGGT	NTXTKYCCCC	1020
SC						1022

## (2) INFORMATION FOR SEQ ID NO:326:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1081 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

MNCGNMNTA TAMAYCWYCT NCACCSGGGA TGNATTGCGG CCGCAATCTT STMASAGAT      60
CTCKAAYTOS GCAMGAMCCG CAGCTATTTG ESTGRASGSE ACCAGCGGGA CCTCCCSGKT      120
CKTTYCTTGC AGRGAGSCKK TGGGTGGGCG CCGTGGCAAT GCCAACCGGC CCCCAAAACN      180
CCGCAAATMY CAAAAACAA CCCSGGGTA GHTCCSGGCC GCCAAATMAA TACCGGTXIT      240
AACCKAGGCN ACSSGCCAAC GSYCCGCCCC AACCAAGGNA CCGTCCGSCC NATAGGYCCG      300
GTGGGGGGCTG CCKTATYKCC AASTCCTCAY CTGNACGGGM CGGYCCMCWT TCCGCCTCAT      360
CCGTCTCTCC TTMATITTC CTCCACAYG GCGGGGAACT TTTTMYCNC CCTTSCMAN      420
CAGCNAGGY CAAAAATTNC CMTGCKKYG SENCAAAYGR GATTGGGTY CGKCTTTTNT      480
TGNMCMAC CCCNTTTNA CCGCCCMATC CCYTNAAGC CCGWMMKMS ANGKTTGNSA      540
AAKYNCCCC AAATGCCAA MYTCTTCCG NTTTMTMCMY YVCTTTCCG CMCCCMRAA      600
GGSCCGCCYY TCGGGAANTY TCCGNCZAA AWTCAMWCM TTTCCNCZA AGAATTCGG      660
SACTCCTTIN TTCNGSGNAM ATANATYTT YCKINGGGSK TTCCSMTCNC AMMAATNTCC      720
AGGGKAAMCC AGKTYNDTCC YYYCCOCAA NNTYCCYEGG KMCYNNYYCY TTAANKLKR      780
SAAGCKSGG GKYNCNCSE TARGCCCMN KAAAATTTCC CCGSKTTTC TYNNKMMRW      840
GCCCCCSAAM ACTMTWAYTT TCCCKCGNN TTSYCCCKG KCMWMMWNG KKNCTTTTNT      900
YCSMATAMA CTYNGSKCT NTENYSSCG CMAAANAAGG CGGGSTTCTN TTNMUMACA      960
YNTSGSMEMA SAARKAWATA AWDNTRKCYK TGNCCCCCCK CKCKCTTSNW TNGCCMCXS      1020
GGGKNWKKR GWCTCCWNC CCCCCCKGK CCKWATMCC CCCCCKCCM NCHSTTTTNT      1080
CCC

```

1083

## (3) INFORMATION FOR SEQ ID NO:327:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1069 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

## (2) MOLECULE TYPE: GENOMIC DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

```

GGGGNKKYAT MCAYCWTCTE YACGGGMMN TATTGCGGCC SCANYTNGTM GASAGATCTC      60
GAAYTOSGCA MGAATAAGW GATGTGCTGG ACCTTMCSC GCGGACCG ACCRACAAG      120
RAASCSCGCC ANAATATTGG CCACANTTGG TCACATATTT ACCCAATTMT AYCAGGGAYT      180
MCCATTCCKG GAGACRACCG CACATCCCR ATSTYGGTFT SCRAACCTR ACGTCCCCA      240
MYTYGCCERA STTGAAACCAG GGCRAAAAR CCGCCRAAY CTGCGCCTGA NTCCGCTCE      300
GCGCNAAIAA CTAGGCCCAT TXAAGGAAC CGNGGCCSC NANTTGGCCA ACRGCTCTR      360
ACAAAGGGGC CCCTATYGGG CCGGWTCCW TTYCACNCC TMTCTCTG CCGAATYCG      420
WTCRAZNYC CWTGSGCT TKCKYCKYC KYCGGTMCA AWCTNGCTA TNCATREK      480
TCCCTAARAT SCNAICTGG GCHYCCATT NCTGGNTTC NATTTAMMAN SRGCGTTCT      540
TTCTTCCRA AACCGSNTGG CCGNMCCA AAAATGATN ATAATAATGK YGCTTTCAC      600
ACCCGCCCC CCCTTCRWT CGGTCCANC CCGNNGGT TAAGTYGGA ATTTTNAMC      660
YCNAGSCCT NATTTGGNA AAAACCYCY GGYCTCAA CMYTTTTT GSKSNTCCG      720
GCTCTTCSC CAARAACCAA ATNTYNYGG GGYCKTNA AEMCGGYCR RCGGAAT      780
TTTTTGGTTC AACCCCAACC TTYTCAACC NTTTTTYT TCCSSCMN TNGSGGNT      840
KSSCNTTCY RAREKCCNM GGGGMYCYM CCCCMMYTT CTTTTTTTTT CGTSMULAN      900
NGXTTCTTCA AAMCCCCC SCGCCNSAA ACCCGTNAR GTTTTYOMA AANNWYNGN      960
KNCCTCCCCC MNAATAAAY YSCCGGWN ACMSNNGGA MCCCCCGSN NTKATTTTT      1020
TNCAGYCC CSMASYTT TKAMAMNRK GAGNTTNTY TNNKNNKX

```

1069

## (2) INFORMATION FOR SEQ ID NO:328:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1310 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

```

NGNGGGGKWK MATAACATCWT TCTTCACGSG GGATCWATTG CGGGCCGCAW TCTMGTMCAA      60
SAGATCTCCA TYTCGGSCAM NACCCACGWC TCCRAAAAAA ACCCRAAWCT CGGGSKCTYC      120
GARAAGTGTG GCCCGCKTR AATTTAACAA ATTCAGTGTG ANAGTGTGAC GGCKTTACWT      180
YCCCGGCAAA GGGGGCCACAA CCTGCAGRGA SCACYCRATG GKTGYTGTG CNGGGGCGGC      240
CCGGKTHAAG GGACCTGCTT GGGTGTGCSG TNCAAANATC WYCGGCGGCT YCGCTGKRAT      300
MCNCAGGGGT GTCAAAAAAC CGCAACAGG CACGCCANCC NTTTACGGGG CTTAAAANGA      360
AAAAGGGGCTG ATGCCCCGAA GGGGGCGCGG NCCCAACCTT CGGTTGGTCA ACAACCGGCT      420
CTTCTGKTCG RAATCGGRHT CCRATHYCGC GWTCGCGTTC TCKYCTYCTV CGGTACCCAA      480
ATCTGGGTAT CCTATASTGT CCCCCAANTT CCAANTCTGG GCTGTCCATY TGGTTGGCNT      540
TCCAAATTTA CCANCAACGG TTTCTTNCAT NCCAAAAACG GNTKGCKKCC NRACCCRAAA      600
AAATGAATAA TATAAHNGG KGNNTTYCNA ACCNCCCCCC CCNATTCCA TYSNGTTCCA      660
NMNCCCCCAG NGGKTAGGTX GGGAAANYYC TCMACCCYCA ANCCCTWARS TTTTNGRAAT      720
KAAACCCCTC YCNGGGTCWW TYMAAAAMA NTTATTTGGM NGNTTTCGGG MNWCKRKHST      780
SCCAAAATCC MAAATANTTT YTTGGTYCNA TWAAAAAMCG YGNCNCCGCC GGAAAAWTTT      840
TTNTGKTTSA ACCCCAAAAC YTTTTCMNA NCSKTTTTY CTTCCCCCCC AMNWTGGGYS      900
GGGNATKGYG SCYTNTCTTA TXTKYTYMTW CMGGGGGGNN KMTTCMMCCC CCHTTTTYCY      960
NYWRTTTTTN KCCCCXTNMR NIRAANNNGN YTCYNANAA AAGCNCCCCC SCCNCCCNNA      1020
AAAANCCCCN NNIRAKTNT TTMKANRNMN SCKCNKNGKY YCCCCCCGWC YNMNMAAAAA      1080
AATMYCCGNC BASAHMCASH NMCGRGNRSC CCCCCCCTT NNNNTMTDNT TTTTTCERA      1140
GAGCKCCSCG MNMAHMCNCK CTTTTTKCNC NNNNNNNNNN GNGMNCNCC CCNAGAAMWE      1200
CTKSTCCSYG                                     1210

```

## (i) INFORMATION FOR SEQ ID NO:329:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

```

NGSEENGNNA TMCATCWYCT GYACGGGGMT CWATTGCGGC CGCAACTNGT MAASAGATCT      60
CGAAYTCGGC AAKAWACACC ACCGCGGTGT MTATACACCG CAAATGTTCT GTKTGCCAAA      120
ACCGAGACGC GCCGGCCGCG GGGYTCCAAC GKTTTACTYR ACCCGCCAGY TCAGTGTTEA      180
AACCGGTGTT RAAGGGCCGCA CCCAACWTA ACGCTTTAKE CAAGRANYTG GKTGGGCGGC      240
AGCCACCTGY TGTGGYTGCC CTCWYCGGTG GTAGCGCCCG TTANCGGCGG TTGCGCGYTC      300
AMCASCSCGC CGGTATGCCC AKCNWTCGCC CGGCCMRACC CACCGGSCAC TTTGRACGGT      360
GCCGGCAATT CAAAYCKYCT GRWTGCTTCM AAACACCACR AAGGCTACCM CCMSCACCMN      420
ATMGGGRACT TTAAGGCCCC GGCAAAACCT NTRAKNGCT CCGGGGCRAA GGTCCGSCAA      480
SCRATCCMAA AAAAKCNAT TTCCCCAGC AKCAACCTAA MCGGTTTTGC TGCTTCGGHA      540
TTCCAAMCCA ATTMCWGGKT NCNWGGGAAA AACASCNCC NTAKECMG CCMCGGSCA      600

```

ATTTCSERAA	SAACCCCTNY	CCCGGTTTT	YCCTGCTCMG	GCCCAANACT	CCCGGGAATC	660
AAAAAAGGTC	GCNCAAANGG	GCMAAACCCS	SACCCMACTT	WTTCCRCCTN	GGGGGGGCMN	720
CCKNGTTTAA	ANKSCCTCY	CTSCCCAAAY	TGSEKCMAAA	NNGRKTTGGK	TINGGCMACC	780
NTTTCGGGKC	CCCGGGGKGE	WKKYCTMMA	CSYTTNTTTT	SCCCCYKAAA	NYSCCCCCCC	840
CGGSSCCCCS	CCCGGGGGGA	NNTTTTTAMA	GKNTYCCCC	CCCCAMAAAA	ANACCCNYC	900
CCSGGSCCCT	ITRWAAAMN	KCTSCCCGNG	GNNGGGGKCM	GGKTTATTMT	NNNCCSCCCC	960
TCCGCGSAAA	AAATAKMTT	SYCCCCCNC	CTCKNCKNR	GKAMMSCCG	TCCCYCTCNC	1020
GCKNTWAAN	ARNCCKKNN	CCNCYKCCS	NNGKCNWCD	NCCSTSNCT	NKGCNCKCN	1080
KAAANAAYNC	NGSMSTSSMN	CNKCC				1105

## (2) INFORMATION FOR SEQ ID NO:330:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

NGSNNKNNK	TAMAYCWYC	TSCACNCGA	ACWANTCCG	CCRMAMCTNS	TMKASAGATC	60
TMGAAYTCG	CAAGAGCGGC	AAGAGTGTOT	GCATCTGGTC	ANAGTSTMMA	CRGGGTGCCG	120
CSGGTGKOTR	GASCACMCAT	NTGCRACAC	CAAAACCKTC	GCGGGYCAC	GGCNTCCCT	180
GCAAAWYCC	CCAGGCCACT	TCRAACMAW	YCTYCTGCA	CCARGCCCT	TYCGCGGCCG	240
RATCCGTGKT	CASYVCCCK	TCCGTGCCC	AAGKTACTCG	CSAYCAAAA	CCGCTCCCGG	300
RAACRAACKT	AAWTYCCCG	AAATTGNTTC	CCCTGCCCT	TGATAAATTT	NTNAAGCCAC	360
CGCAAMCCTY	CGGGCKTCT	CTCKTGCCRA	ATYCBRTCC	RATAYCCCA	TGGCCTNKT	420
KYCTYCKYCS	GTACCCAAAT	CTTGCGTATC	CTATANTHYC	CCWAAANECA	AWTCTGGGCK	480
KTCATHTSC	TGGSKTCRA	ATTAMMACA	NCGGTTTCTT	TCWTACAAA	AACGNTGGG	540
CGGCRACCA	AAAAGGATA	TAATAAKGTG	CWNCRAAAC	CCGCGCCGCG	RRTTCAAYCG	600
GTCCARCACC	CCANGNGGTN	AGSTNGGAT	TYTMAACCC	CAGCCATRA	SNTTNSGNAA	660
AAACCCGCCN	GGGYMYCAA	AMMCTTTTTG	GGGNTTCCSG	CCATNGYKCC	AAAACCAAAA	720
TMTTTCVGGT	GNWAAAACC	GGCCGCCCCG	NAAATTTTTT	GKCAACCCCA	AACCTTTMAM	780
CCNNNTTCVY	YCCNSACAA	TNGGSGGNKN	NGSSCNTTYT	TWTTTYNNNA	GGGGGRRWC	840
SNCCCCNAAN	YCCNAAANK	NKCCCGNMA	AAAGAGANTT	YCNKAAAAAC	CCCCCNCCT	900
KAAAYACCCC	MAAAKWTTCN	AAASMSCHNG	YCCCCC			936

## (2) INFORMATION FOR SEQ ID NO:331:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1042 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

NNNNNNNNNY	ATMMAYTCWY	YCTSCACCCG	GGNNWCWATT	GCGGCCCMAN	KOTTGTMAAS	60
AGATCTMBAA	YTCCGACAG	ASSGACACAG	ASCGCGGGCG	CTATYCHYCC	GYTGCTCATG	120
CTCAACACCC	TCTTGGGCGW	GRATAATGCC	NCGCCGCCCG	CCCAACACG	YTCAYTGGCT	180
TGCCCAACCC	CATATNTCAA	CAGGTRATA	AAASCAAAAC	CGCSCCTCY	GCCCCTGGGC	240

SCGGRAASCG	CTGCCAACCC	RAAACNCKTY	GGGCACYCGG	KTSRACTTTA	AASGGTAATC	300
TCKTCCTCCT	GGGCTATGGT	GGCCACACAA	CCTSYTGGCG	WGGGTCTGGC	CCTGGGYCAC	360
CGYCRCTTTT	TAINTNTCK	YCTACACNCT	TKGGTYCAAC	CACTCCACTT	CACMAAATTG	420
TTTTGGGKTG	GGGSGGCGG	YTGTNNCCGK	TAATAATCGG	MTGKTCGGCC	MYCACCGGWA	480
CCATANGCTG	GGGGGCSCTG	GCAAAATTTC	SAAATCATYT	CCTTCTGRAC	CCCCACAMEC	540
CTNSAAATCC	GRATCAATNC	CCCNKGGCTT	NTCYCTCTCN	GTRCCCAATY	TGGTTTCTAT	600
RKTNCCSYAA	TSCAATTGGS	TTYCCRTTSC	YGSTTCCAAN	TTNACAAMAE	GGTTTTCTMT	660
ACCAAAACCC	NTGGSCCNNA	CMNAAAAAGN	BAAAANAKGG	KCTTTYAAAC	CCCCCCCTAT	720
TCAWYCGGTN	CMRNWCCCGG	NGKAAGGKEN	GAAAYTTHER	CCCAANCCMT	ARSTTGNNAE	780
AAACCTTYCG	GGGTSMCAAA	MENYWTSSC	CTTCGGMCTT	YCCAAATMSA	AAATYYTCKE	840
KRMNAAAAAC	YGNCCDCBAA	ANATTTTTGT	NAAMCCCKMA	YFRTTWMCC	WTITTCCTCC	900
CCCNHNSNSG	GNTNCCCTTY	TYATTTCYMM	MCRNNSGACN	CCCCMFTYTT	TWTTCKCNEN	960
MMARGSMRYT	RGRMSMNC	CCNCCCNNAE	MTCCNCAAAK	MTTINAACNN	NMKYCKCCTC	1020
CCCNMNNKNC	CCCNMNCMTT	TM				1042

## (2) INFORMATION FOR SEQ ID NO:332:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO:332:

NNSGSGMKKK	ATAMATCWCT	CTSYACCENS	GMTGWATTGC	GGCCGMATWC	TNGTMAASAG	60
ATCTCGAAYT	CGGCAAAANAK	ACCGMAYGTC	AASTGTTRAY	CGGTACACATA	TCMTCCCGNS	120
TCAACMCCAA	AGCCGNGTCA	CGGYCTCCCT	GGGGCGCCAC	CCCCATCGST	RATGCAACTT	180
CGCGCGCGAC	CGYCAAAAGG	GTCTTTRAGG	CGCTAAAGGT	CAMCAATTC	TRAGGTYNCH	240
CACCGTNTT	TGGCCCGCGC	RAWTYCTRAC	CCGCAATWTC	GGAATTCGG	AATTTGGGCH	300
YCGGCTTGGG	CAATRAAGTN	TTGGGCAAGG	CGGGRWTCYC	NGTGGCCGRA	ATTCCGNCAT	360
TCKTXXAAG	GKTRACCTT	TTYCCCGGTT	GGCTTAAYTG	YTYCTTGGGC	GGCTTCGGCC	420
CRNAGCASY	CECTAACGGY	CMCCAGGCAA	TACCKTTGGG	TTTRAACCCAC	CGGRATHAAY	480
TGKTACCCAC	YTCAAGSGTS	CTGRANTTRK	TNTCTGTRAA	AAAMCCACCN	AACCCGNTTY	540
RATCTGCTTC	MTCANCMITT	SCCGGCTTCT	GGCTTTTTTR	AACTTNATC	CMFYCAAAAG	600
GTITAMTTTC	CCAANRAATT	CGGYTTGCCA	CCTTGGCCCG	GGCTGUTTYM	CGMWCCCTTR	660
AMATCCNCCS	GGCGGSAJAN	AMTTSGGNTT	GGGCGGCTCC	CCGNAATAT	YCTGCGNCTT	720
GNAAATTSSS	GGGATCCGNY	GGNAYCCCG	CCNTKGGGCK	TNCCGCTTG	GWACAATTYC	780
WKCCCTTCCA	AACCCGGGNC	CGGGGGGTGG	GGCCGNTTTT	CCTMYNNAAA	AAGKSTTTGN	840
NYTTTTCGCS	CHRAANTTCA	CCCKNKNTNT	GGNCINAACY	YFYCAANTTC	CANACCTTTA	900
AASAAANCVK	YKTYVCCCG	TTTTMCSSGS	SANCCCCCOM	NMSKNCGGG	AAAAAAAGNE	960
TYNGCCTTAN	CHSKTKTNT	TNTYVCCCGC	NMWNNSNMCT	NCKKCNKRY	NGNSNMNCTT	1020
MTCEKCNHNN	SNNSNKNCGN	GGNCGMYM	CMNCHNGMYE	NGNKNNCCTC	MSC	1073

## (2) INFORMATION FOR SEQ ID NO:333:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GNSNGNNTN	TMCAYCWYCT	SCACSGGGTC	TATTCGGGCC	GCAATVTNGT	CKASAGATCT	60
CGATYTGGGC	AMNANAARTG	TGCTCGTCAA	TTTCAGKKTG	GTCTTCAAAY	GGGCCAGGCC	120
GNGACCRACA	CCCTGNGTCA	CCCAAARNAC	CAACAGCWTC	AAATWTCAAG	GCCRAGGCSC	180
TETCAATYCC	CRASCARKTA	ACCGTKTCCW	TCRAAGGTGC	CRAACCCAGC	ACCCAGYTCA	240
CGCCCSGGCA	AWTCGGGCTG	CCGGCCGGTN	TCAGCCTGAT	TYCTGACCCCT	RWTCTSTSGG	300
TGGYCAMCMT	GGTGAAGGCC	CWCCGCCNA	AGAACTGGAG	GGCRAATTCC	CAGGANCCNA	360
GRAACCCNAG	GAACCCGCCG	TAKAANCCGG	CRAAACCCAG	GGCGYTGGCN	ATTCCNATTA	420
NAMSGGTTTG	CRACNTGGCC	RAACCGTTTY	CTTGGTCCGC	CTCGGCAACC	CTGGACCANT	480
TACCCCKTNC	CCGNNMCNAC	CYGGGGTNGT	TGKYCCCAAT	NTGCTCCCGC	GNNRANTNGC	540
CHAATTCAG	GGCNCNACT	TTCCGGCCCN	AATTGCGYTG	GTEAATCACC	GGCCNCCCT	600
GGTTTGGGC	AACCCNCYS	CTTMTTAA	CATTCCGSCC	CAAATGGGNC	STTGGSAART	660
TCTNTYCGGT	GGGCGGGGCR	ANMYTCTCT	YCCNAASAN	CTTAMYCCAN	TTCGSSNTCC	720
CGGKCAAWS	NGGGGGGNA	AAGGCCCCC	CGGNTSCKCC	GGGGKGGGCC	CYGGKTTCAA	780
AANTTTCGG	GKSTMSGG	NYTCCGCC	CGGCCAAGRA	CCGNGGTTTT	TTTTTGAACC	840
KCMANTCSEA	AMCCGCCSC	CCCNAAAGGS	GCCTNAANGR	RAYTTNKSCC	CNNAAACSGE	900
CCCCCAKTY	SGGKTTGNC	CNCCSGKST	CCMTSTTMM	MRCCCTTTGN	GKKTPTTTAN	960
MGSCCTTNC	CACCCCTYCK	GGGKCCMNNA	GAATMYWEC	CNGGGGNNAN	RSCTCCCCNN	1020
GGGKGGGGK	MGAGYSCCT	CTKCCGNCNN	YKNTTTCCCC	C		1081

## (2) INFORMATION FOR SEQ ID NO:334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GNNNGNNKNN	ATMCAYCWY	CTSCACCSGG	GNTCNATTGC	GGCCGCANKY	TNTMAASAG	60
ATCTMGAAAT	CGGCACANAG	CGGCACAGAG	TGTGTGCATC	TGTGTGANAG	CTGTCAACGC	120
GGTCCCGCSG	GTGGTRASCA	CMCATTGCGR	AACACCAAAC	CCGTCCGCSG	GYCACCGGCK	180
TGGCCTGCAA	AAYCCTCCAG	GCCACCTYCA	AACAAYWYCT	CCTGCAACSC	ARSCTGTTYC	240
GGGGCCGGRAT	CTTGKKYCAS	YTGCCCTTGC	GGTGGGCCAA	GGTACTGGCS	CWYCRANACE	300
GCTYCGGGR	ACCNAAACCTA	AATCTTSCCN	AATTTGCTNT	CCCCCTSCCC	TTTATNAATT	360
TGTTAAACCA	CCCAAACCTY	CGGSCNTCTC	CTCTGCCRA	WTCCGRWTCC	RATNYCGCCA	420
TGGCTNKTIC	KYCTYCKYCS	GTMCDCAAAT	CTTGGTATCC	TATATTGTCC	CTAAATGCAA	480
ATCTKGGCTG	TGCATNTGCT	GGCGTTCAAA	TTWAMANCAG	NGGTTTCTTY	CTTCCNAAAC	540
CCSTTGGCCC	CAAAACNAAA	AATGATNATA	ATAATGCTGC	TNTCAAACCC	CGNCCCATY	600
CNATCSGKCC	AMMCCCCGNN	GGTANXKGG	GNAATTCCTMM	AACCCCAAGC	CATAASNTTG	660
SGANAAACTY	NCNCMGGYCA	SCAAAACANY	NTTNTTGGNY	SENTTCGMMN	YCATGGCTNN	720
CMAAAACCCA	AATACTNYYG	GGYCCAATAA	AAMMMSGGYC	SAMCCCGAAA	WTTTTTTTGN	780
KYNAAACCNA	AAKCTTTTTT	CNAACCCDAN	WNTYCCCTNCC	RCRCMANTGG	CNSGGARTKT	840
SGGCTTMCCT	ATGKYCCMAA	AGNGGGGRANA	CCNACCCCAA	TTCTTNNNTN	KNNCCCNST	900
TKNAAAAGGG	GKNTYNCMAA	AASNCCTNCC	NCNCTGCCAA	AAKAMCCCCN	AAAGAKNTCN	960
NAANASKYSN	NNNSCCCCCC	CCMMNN				996

## (2) INFORMATION FOR SEQ ID NO:335:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

NGNNGGNKEN	ATMAYCWCT	SATYYACCN	GGMMNNAITG	CGGCCRMANT	CTWGTMKASA	60
GATCTMGAA	YTCGGCAAAG	AGYATCTCTG	GGGGCCAGAT	TENTGGCCCC	CAACCGCCGC	120
ACTTTGCAYW	TCAACAKTCC	GGGTCCCCCA	AAAAANTCWT	ACCCCCATMC	TYCTTGCASH	180
ASYTGCCGCC	RATTRAACAC	CGGGCCGGCN	TGCTGCCCA	GGTATTYCAE	CAGYTCAAAY	240
YCTTTKTAGK	TAAATCCAG	CSGGCGGCCA	CNCAGCCGGG	CGGTKTAGST	GCCTYCCTCA	300
ATMACCAGCY	CGCCACGGGY	CACCTTCCCC	AAAAYCTTCT	GGTFCAGCCA	AATTYCCGCS	360
CGGGCCAACH	ACCANCCGCA	TYCTGGCCTC	AATCYCACCG	GGCCCGGTCT	TAAAMMANMA	420
GRATCTCTTC	MANCCCCCAN	TCAGCSYTHA	CNCGMACAGC	CGCCCTTCTT	CAMACCGCCA	480
RTACCGGGWT	CAACCGGCS	GTCAAACTCA	ACAGGCGGNC	AGGCTTCCCC	CGGANSAAAS	540
CTCTTTACSC	NNYAANAAAA	MAAGTCTGT	TTTCCCCCTC	CASAASNAAS	AANCCCCSGC	600
CGGGCCCTTCN	NNMGCGTTTG	GGMANANRA	AARCNCCGNC	GGACCNATC	CGAAAMCTCC	660
CAAGTCNCMT	FWAAACYCN	NNAACCCGCC	ANTTTTGGGA	AAGGNTCCCC	NTTMYCCCCC	720
TTTTASGKTS	CGMMFYCTY	TAAAAAATT	CCCCAAAAAG	CCCCGGGAAG	GGTCMAMCTG	780
GGNAAATTTT	CAAMCCMWK	TTNTTYNGGT	TMCGGGGGGA	AATTYCNCTC	CCYYNNNGGG	840
CSGGSNNNAT	TAYGMSNMT	TTTNMAATM	NSGKKTSAAM	YNNKCCNNNN	NNNMMAHNNK	900
TNAMCKCCCN	CCTCNGNGKY	CSYNNCCSCG	CNAGNGGRAS	MKCCNAMMAA	AYASGNTTHK	960
CGGAAMCCNN	AATKGNTRSC	CGGASMCNN	NNNMAAATMT	CNCHKCNENN	AANRGMRACN	1020
CCCNNSGMM	NSGAARMTHY	YCCCCCGSKM	GKGNKAAAN	GKYCCCCCCM	AAAG	1074

(3) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

NGNGNCNEFT	MTACATCWT	CTCACCCSGG	GNTCWANTGC	GGCCGCANFY	TTGTGASAG	60
ATCTCGAAT	CGGCAMGAGG	ACNCTCCRA	CGCCCCACA	NACTCTGCGG	TGTGTACCCC	120
ATTGNGCGCK	TCACCGCCCC	ATCGANCCAK	TNCATCGGGG	TGCCCTYCCG	CKTGGCCGCG	180
GGCCTCACGG	CKCTSCWTCY	RAAGGCWTGG	CGCACCCGAT	TGGTTTCT	RAACGCTGGG	240
AAAWTGGCCA	GGCCTCTGGC	TCATGGGNTC	TACGCAACCC	CNCGCCCCAA	CRCTTTCTTA	300
AATCCGTYCC	NTCCTGANC	CTTGAAYCC	CGGGGSAAGA	ACTGGTTGCS	CNCGAYCTGC	360
TCGAACTTCK	TCNAAATCCC	GCANAKTETT	TCNTAMGYCC	CNCGGGAAGG	NGAACCTACT	420
TTCTGGWANG	TCUGCNKCCC	CGGCTTATCA	ETCCTGATCA	ACGGGGAAGT	GGYXNNSTTS	480
KGGGAAAAAG	RRCTTCAATG	MTYGGTCCCK	GCTGCGKANC	CGGSCCTGK	GYCGCNAATG	540
GAAGGCCMAG	GGTTAANGCC	MTTYCNYYCC	RSCCTSTCA	SGKWTTYCCG	MGGANKAMNN	600
NNKMAMWTTK	TCRNGGGCCN	ATSTSCCGGG	CKSTTAKAGA	ANACTYCCXW	WCCGTNTYSC	660
SAAAGNTXCS	GGCMGTTTTT	SGCNMEANGN	YCTGATTTSA	GGGGGKYKCC	CGCGGGSTYC	720
CGAANENRKY	CCYAGGGGGM	GNYSAGCSC	CGGNHATNAC	AGNAAGGKTT	RYGSTSKNCC	780
TYTNYGGACC	WSCNHCWBAK	ANAACNNKCT	TGCSCCNTMS	AGNKTNRKRT	YCCNKTSTTC	840
TACAGGAGCC	TATMKCCCC	CTTGGAGGMM	GAGWEMGCCG	KYCCCNKRT	TCNTNGWAAA	900

TATTAAGMGG	TECCGMAOMK	CCSCGTTTKT	TKTGANAAMN	MEMBKNNKTC	CGMGYTTCTSC	860
GGGNTTTTOTA	GAGTAKTCGS	CCSCSMWGAC	WCSCMCMGNG	AGKNTNNTS	YANTGARCXY	1020
MNNEKTMOMT	MSCSCGCGNA	GGAGNGCCCC	CSANGMSTGY	NKGNMSSNG	ABAKGATGGS	1080
GGCCNCGMNN	MGMGGANMGA	SAHNGMGGMR	GGGCGKTKGC	TCKSCCGNS	CSANGRAGAA	1140
GKTCNGSGCC	CGMGCKYKNT	KTKTKNHTGG	YSTCMSSMM	NAGAAAAGAG	AGGCG	1198

## (2) INFORMATION FOR SEQ ID NO:337:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3872 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

CCATCTGATC	GTTCGCAACC	AGCATCGCAG	TGGGAACGAT	GGCTTCATTC	AGCATTTGCA	60
TGGTTTGTTC	AAAACCGGAC	ATGGCACTTC	AGTGGCTTTC	CGTTTCCGCT	ATCGGCTGAA	120
TTTGATTCGG	AGTGAGATAT	TTATGCCAGC	CAGCCAGACG	CAGACGCGCC	GAGACGAAAC	180
TTAATGGCCC	CGCTAACAGC	CGGATTTGCT	GGTGACCCAA	TGCGACCAGA	TGCTCCACGC	240
CCAGTCGCGT	ACGCTCTTCA	TGGGAGAAAA	TAATACTGTT	GATGGGTGTC	TGGTCAGAGA	300
CATCAAGAAA	TAACGCGGSA	ACATTAGTGC	AGGCAGCTTC	CACAGCAATG	GCATCCTGGT	360
CATCCAGCGG	ATAGTTAATG	ATCAGGCCAC	TGACGCGTTC	CGCGAGAAGA	TTGTCCACCG	420
CGGCTTTACA	GGCTTCGACG	CGGCTTCGTT	GTACCATCGA	CACCAACACG	CTGGCACCGA	480
GTTCGATCGC	GGGAGATTTA	ATCGCCGCGA	CAATTTGCGA	CGGCGCGTGC	AGGCGCAGAC	540
TGGAGGTGGC	AACGCCAATC	AGCAACGACT	GTTCGCCCCG	CAATTGTTGT	GCCACCGGCT	600
TGGGAATGTA	ATTGAGCTCC	GCCATCGCCG	CTTCGACTTC	TTCCCGCGTT	TTGGCAGAAA	660
CGTGGCTTGC	CTGCTTCAGC	ACGCGGGAAA	CGGTCTGATA	AGGACACCGG	GCATACTCTG	720
CGACATCGTA	TACGTTACT	GGTTTCACAT	TCACCAACCT	GAATTGACTC	TCTTCCGCGC	780
GCTATCATGC	CATACCGCGA	AAGGTTTTCG	GCCATTGCGT	GCTGTCCGCG	ATCTCGACGC	840
TCTGCTTTAT	GCGACTCCTG	CATTAGGAAG	CAGCCCGAGT	GTAGGTTGAG	GCCTTTCAGC	900
ACCGCGCTTC	CAGGGAATGG	TGCATGCCAG	GAGATGGCGC	CCAACAGTCC	CCCGGCGACG	960
GGGCTTCCCA	CGATACCCAC	GGGAAACAAA	GCCTTCATGA	CGCGGAAGTG	CGGAGCTCGA	1020
TCTTCCCCAT	CGGTGATGTC	GGGATATAG	CGCCACGCAA	CGCACCTGT	GGCGCGCGTG	1080
ATGCGCGGCA	CGATGCGTCC	GGGCTAGAGG	ATCGAGATCT	CGATCCCGCG	AAATTAATAC	1140
GACTCAGTAT	AGGCGAATTG	TGAGCGGATA	ACAATTCGCG	TCTAGAAATA	ATTTTGTTTA	1200
ACTTTAAGAA	GGAGATATAC	ATATGGGCGA	TCATCATCAT	CATCACGTGA	TGGACATCAT	1260
CGGACGAGC	CCGACATGCT	GGGAACAGGC	GGCGGCGGAG	GGGTTCCAGC	GGGCGCGGGA	1320
TAGCGTCGAT	GACATCGCGG	TCGCTCGGCT	CATTGAGCAG	GACATGCGCG	TGGACAGCGC	1380
CGGCAAGATC	ACCTACCGCA	TCAAGCTCGA	AGTGTCTTTC	AAGATGAGGC	CGGCGCAACC	1440
GAGGGGCTCG	AAACCACCGA	GCCTTCGCGC	TGAAACGGGC	GGCGCGCGCG	GTACTGTGCG	1500
GACTACCGCC	CGCTCGTCCG	CGGTGACGTT	GGCGGAGAGC	GGTAGCAGCG	TGCTGTACCG	1560
GCTGTTCAAC	CTGTGGGGTC	CGGCTTTTCA	CGAGAGGTAT	CGGAACGTCA	CGATCACCGC	1620
TCAGGGCACC	GGTCTGCGTG	CGGGGATCGC	GCAGGCGCGC	GGCGGACGCG	TCAACATTGG	1680
GGCTTCGAGC	GCCTATCTGT	CGGAAGGTGA	TATGGCGCGG	CACAAGGGGC	TGATGAACAT	1740
CGCGCTAGCC	ATCTCGGCTC	AGCAGGTCAA	CTACAACCTG	CGCGGAGTGA	GCGAGCACCT	1800
CAAGCTGAAC	GGAAAAGTCC	TGGCGGCGAT	GTACCAGGCG	ACCATCAAAA	CTTXXGACGA	1860
CGCGCAGATC	GCTGCGGTCA	ACCGCGGCGT	GAACCTGCGC	GGCACCGCGG	TACTTCCGCT	1920
GCACCGCTCG	GACCGGTCGG	GTGACACGTT	CTTGTTCACC	CAGTACCTGT	CCAAGCAAGA	1980
TCCCGAGGGC	TGGGCAAGT	CGCGCGGCTT	CGGCACGACC	CTGACTTTCC	CGCGCGTGGC	2040
GGGTGCGCTG	GGTGAGAAAG	GCAACGCGCG	CATGGTGACC	GCTTTCGCGG	AGACACCGGG	2100
CTGCGTGGCC	TATATCGGCA	TCAGCTTCCT	CGACCAAGGC	AGTCAACGGG	GACTCGGCGA	2160
GGCGCAACTA	GGCAATAGCT	CTGGCAATTT	CTTGTTCGCG	GACCGGCAAA	GCATTGAGGC	2220



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CCCCGGCGGT GCGTTCCCAT CGAAAACCCC GCGGAACCAG GCGATTTTGA TGATCGACGG 2280
GCCCCCCCCG GACGGCTACC CGATCATCAA CTACGAGTAC GCGATCGTCA ACAACCGGCA 2340
AAAGGACGGC GCCACCGCGC AGACCTTGCA GCGATTTCTG CACTGGGCGA TCACCGACCG 2400
CAACAAGGCC TCGTTCTTGG ACCAGGTTCA TTTCGAGCGG CTGCGGCGCG CGGTGGTGAA 2460
GTTGTCTGAC GCGTTGATCG CGACGATTTC CAGGCTGAG ATGAAGACCG ATGCGGCTAC 2520
CCTCGGCGAG GAGGCAGGTA ATTTCCAGCG GATCTCCGGC GACCTGAAAA CCCAGATCGA 2580
CCAGGTGGAG TCGACGGCAG GTTCGTTTGA GGGCCAGTGG CCGCGCGCGG CCGGGACCGC 2640
CGCCGAGGCC GCGGTGGTGC GCTTCCAAGA ASCAGCCAAT AAGCAGAAGC AGCAACTCGA 2700
CGAGATCTCG ACGAATATTC CTCAGGCCCG CGTCCATAC TCGAGGGCGG ACCAGGAGCA 2760
GCAGCAGGCC CTGTCTCTGC AAATGGGCTT TCGATTGAG TTGCGGCTGC CTCTGGCTG 2820
GCTGGAGTCT GACGCGCGCG ACTTGAGTA CGGTTGAGCA CTCTGAGCA AAACCACCGG 2880
GGACCGGCGA TTTCGCGGAC AGCGCGCGCG GGTGGCCAAT GACACCGGTA TCGTCTCGG 2940
CGGCTAGAC CAAAAGCTTT ACGCCAGCGC CGAAGCCACC GACTCCAGG CCGCGGCGCG 3000
GTTGGGCTCG GACATGGGTG ACTTCTATAT GCGCTACCGG GGCACCGCGA TCAACCGGA 3060
AAGCTCTCTG CTYGACCGCA ACGGGGTGTC TCGAAGCGCG TCGTATTACG AAGTCAAGTT 3120
CAGCGATCCG AGTAAGCGCA ACGGCCAGAT CTGGACGGGC GTAATCGGCT CCGCGGCGCG 3180
GAACCGACCG GACGCGCGCG CCGCTCAGCG CTGGTTTGTG GTATGGCTCG GGACCGCGCA 3240
CAACCGGCTG GACAGGCGCG CGGCCAGGCG GCTGGCGGAA TCGATCGGCG CTTTGGTCTG 3300
CGCGCGCGCG GCGCGCGCGG GGGAGGTGCG TCTTACCTCG ACGACCTCGA CACCGCAGCG 3360
GACCTTACCG GCTTGAGAAT TCTGAGATA TCCATCAGAC TCGCGGCGCG TCGAGCAGCA 3420
CCACCGACCG CACTGAGATC CGGCTGCTAA CAAAGCGCGA AAGGAAGCTG ACTTGGCTGC 3480
TGGCACCGCT GAGCAATAAC TAGCATAACC CTTTGGGCGC TCTAAACGGG TCTTGAGCGG 3540
TTTTTTGCTG AAAGCAGGAA CTATATCCCG AT 3572

```

## (2) INFORMATION FOR SEQ ID NO:338:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```

Val Gln Phe Gln Ser Gly Gly Asp Asn Ser Pro Ala Val Tyr Xaa Xaa
1           5           10           15
Asp Gly Xaa Arg
20

```

## (2) INFORMATION FOR SEQ ID NO:339:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

```

Thr Thr Val Pro Xaa Val Thr Glu Ala Arg
1           5           10

```

## (2) INFORMATION FOR SEQ ID NO:340:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Thr	Thr	Pro	Ser	Xaa	Val	Ala	Phe	Ala	Arg
1				5					10

## (2) INFORMATION FOR SEQ ID NO:341:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Asp	Ala	Gly	Lys	Xaa	Ala	Gly	Xaa	Asp	Val	Xaa	Arg
1				5							10

## (2) INFORMATION FOR SEQ ID NO:342:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Thr	Xaa	Glu	Glu	Xaa	Gln	Glu	Ser	Phe	Asn	Ser	Ala	Ala	Pro	Gly	Asn
1				5					10					15	
Xaa	Lys														

## (2) INFORMATION FOR SEQ ID NO:343:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

CTAGTTAGTA CTCAGTCCCA GACCGTG

27

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GCAGTGACCA ATTCACTTCG ACTCC

25

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2412 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

CATATGGGCG	ATCATCATCA	TCATCACCTG	ATCGACATCA	TGGGACCCAG	CCCCACATCC	60
TGGGAACAGG	CGGCGGCGGA	GGCGGTCCAG	CGGCGGCGGG	ATAGGCTGGA	TGACATCCGC	120
GTGCTCTGGG	TCATTGAGCA	GGACATGGCC	GTGGACAGCG	CGGCGAAGAT	CACCTACCGC	180
ATCAAGCTCG	AAGTGTCTTT	CAAGATGAGG	CGGCGGCAAC	CGAGGGGGTC	GAAACACCGG	240
AGCGGTTGGT	CTGAACCGGG	CGCGGCGCGC	GGTACTGTGG	CGACTACCGC	CGGCTCTGGG	300
CGCGTCACTT	TGGCGGAGAC	CGGTAGCAGC	CTGCTCTTAC	CGCTGTTCAA	CTGTGTGGGT	360
CGCGGCTTTT	ACGAGAGGTA	TCCGAACCTC	ACGATCACCG	CTCAGGGCAC	CGGTTCTGGT	420
CGCGGATCG	CGCAGGCGCG	CGCGGGGACG	GTCAACATTC	GGGCGTCCGA	CGCTATCTG	480
TCCGAAGGTC	ATATGGCGCG	GCACAAGGGG	CTGATGAACA	TCCGCTTAGC	CATCTCGGCT	540
CAGCAAGTCA	ACTACAACCT	GCGGGAGTGG	AGCGAGCACC	TCAAGCTGAA	CGGAAAGTTC	600
CTGGCGGCGA	TGTACCAGGG	CACCATCAAA	ACCTGGGACC	ACCGGAGAT	CGCTGCGCTC	660
AACCGCGCGG	TGAACCTGCG	CGGCACCGCG	GTACTTGGCG	TGCACCGCTC	CGACGGGTCC	720
GGTGACAGCT	TCTTGTTCAC	CCAGTACCTG	TCCAGGCAAG	ATCCCGAGGG	CTGGGGCAAG	780
TGCGCGGCGT	TGGGCAACAC	CGTCGACTTC	CGGCGGCTGC	CGGCTGCGCT	GGGTGAGAAC	840
GGCAACGGCG	GCATGGTGAC	CGGTTGCGCC	GAGACACCGG	GCTGCTTGGC	CTATATCGGC	900
ATCAGCTTCC	TGCAGCAGGC	CAGTCAACCG	GGACTCGGCG	AGGCCCCAAT	ACGCAATAGC	960
TCTGGCAATT	TCTTGTTCGC	CGACGCGCAA	AGCATTCAAG	CTGCGGCGGC	TGGCTTCCCA	1020
TGAAAAACCG	CGGCGAACCA	GGCGATTTGG	ATGATCGAGC	GGCGCGCGCC	GGACGGCTAC	1080
CGGATCATCA	ACTACGAGTA	CGGATGCTTC	AACAACCGCG	AAAAGGAGCG	CGGACCGCGG	1140
CAGAGCTTGG	AGGCAATTTCT	GCACTGGGCG	ATCAGCGAGC	GCAACGAGCG	CTGTTCTCTC	1200
GACGAGGTTT	ATTTGAGCGC	GCTGCGCGCG	CGGCTGGTGA	AGTTGTCTGA	CGGCTTCATC	1260
CGGACGATTT	CGAGCGCTCA	GATGAAGAGC	GATGCGGCTA	CGCTGCGCGA	GGAGGCGAGT	1320

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AATTTGAGGC GGATCTCCCG CGACCTGAAA ACCCAGATCG ACCAGGTGGA GTCCACGCCA 1380
GTTTCGTTGC AGGCGCAGTG GCGCGGCGCG GCGGGGACCG CCGCCCAGGC CGCGGTGGTG 1440
CGCTTCCAAS AAGCAGCCAA TAAGCAGAAG CAGGAACTCG ACCAGATCTC GACGAAATAT 1500
CGTCAGGCTG GCGTCCAATA CTGAGGGCCG GACGAGGAGC AGCAGCAGGC GCTGTCTTCG 1560
CAAAATGGGCT TTGTGCCCCA AACCGCGCGC TGCGCGCGGT CGACCGCTGC AGCGCCACCC 1620
GCACCGGCGCA CACCTGTTCG CCGCGCACCA CCGCGCGCGG CCAACACCGC GAATGCGCCG 1680
CGCGGCGGATC CCAACGCGAG CCTTCGCGCG GCGGACCGGA ACCGACCGCG GCGACCTGTC 1740
ATTGCGGCGCA ACGCACCGCA ACCTGTCCCG ATCGACAACC CGGTTCGAGG ATTCAGCTTC 1800
GCGGTGCTTG CTGCTGCGGT GAGTCTGAC GCGCGCGACT TCGACTACCG TTCAGCACTC 1860
CTCAGCAAAA CCACCGGGGA CCGCGCATTT CCGGACAGC CGCGCGCGGT GCGCAATGAC 1920
ACCGATATCG TGCTCGCGCG GCTAGACCAA AAGCTTTACG CCAGCGCGGA AGCCACCGAC 1980
TCCAAGGCGG CGCGCGCGGT GCGCTCGGAC ATGCGTGAAT TGTATATGCC CTACCGCGGC 2040
ACCGGATCA ACCAGGAAC GGTCTGCTC GACGCGAAG GGTGTCTGG AAGCGCTCG 2100
TATTACGAAG TCAATTGAG CGATCGAGT AAGCGGAAG GCGAGATCTG GACGCGCGTA 2160
ATCGGCTCGC CGCGCGCGAA CGCACCGGAC GCGCGCGCGC CTCAGCGCTG GTTGTGGTA 2220
TGCTGCGGGA CCGCAACAA CCGGTGAGC AAGCGCGCGG CCAAGCGCGT GCGCGATCG 2280
ATCGCGGCTT TGCTGCGCGG GCGCGCGCGG CCGGACCGG CTCTGCGA GCGCGCTCG 2340
CGCGCGCGCG CGCGCGCGGA AGTCTCTCT ACCCGACGA CACCGACAG GCGCGGAGC 2400
TTACCGGCT GA
2412

```

## (2) INFORMATION FOR SEQ ID NO:346:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 902 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

```

Met Gly His His His His His Val Ile Asp Ile Ile Gly Thr Ser
1      5      10      15
Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg
20     25     30
Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met
35     40     45
Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val
50     55     60
Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser
65     70     75     80
Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro
85     90     95
Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr
100    105    110
Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn
115    120    125
Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln
130    135    140
Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser
145    150    155    160
Gln Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala
165    170    175
Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His

```

180	185	190
Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile		
195	200	205
Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn		
210	215	220
Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly		
225	230	235
Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Gln Gly		
240	245	250
Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val		
255	260	265
Pro Gly Ala Leu Gly Gln Asn Gly Asn Gly Gly Met Val Thr Gly Cys		
270	275	280
Ala Gln Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp		
285	290	295
Gln Ala Ser Gln Arg Gly Leu Gly Gln Ala Gln Leu Gly Asn Ser Ser		
300	305	310
Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala		
315	320	325
Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp		
330	335	340
Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Gln Tyr Ala Ile		
345	350	355
Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala		
360	365	370
Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp		
375	380	385
Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp		
390	395	400
Ala Leu Ile Ala Thr Ile Ser Ser Ala Gln Met Lys Thr Asp Ala Ala		
405	410	415
Thr Leu Ala Gln Gln Ala Gly Asn Phe Gln Arg Ile Ser Gly Asp Leu		
420	425	430
Lys Thr Gln Ile Asp Gln Val Gln Ser Thr Ala Gly Ser Leu Gln Gly		
435	440	445
Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg		
450	455	460
Phe Gln Gln Ala Ala Asn Lys Gln Lys Gln Gln Leu Asp Gln Ile Ser		
465	470	475
Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Gln Gln		
480	485	490
Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala		
495	500	505
Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro		
510	515	520
Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro		
525	530	535
Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro		
540	545	550
Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn		
555	560	565
Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Gln Ser		
570	575	580
Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr		
585	590	595
600	605	610
615	620	

Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr  
 625 630 635 640  
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu  
 645 650 655  
 Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu  
 660 665 670  
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Glu Glu Thr Val Ser  
 675 680 685  
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys  
 690 695 700  
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile  
 705 710 715 720  
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp  
 725 730 735  
 Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala  
 740 745 750  
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro  
 755 760 765  
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala  
 770 775 780  
 Gly Glu Val Ala Pro Thr Thr Thr Pro Thr Pro Gln Arg Thr Leu  
 785 790 795 800  
 Pro Ala

## (2) INFORMATION FOR SEQ ID NO:347:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Other

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GGATCCAAAC CACCGAGCGG TTCCCTGAA ACCG

34

## (2) INFORMATION FOR SEQ ID NO:348:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Other

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

CCCTCCGAAT TCACCTCCGG AGGAAATCGT CCGGATC

37

## (2) INFORMATION FOR SEQ ID NO:349:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1962 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

```

CATATGGGCC ATCATCATCA TCATCAGGGA TCCAAACEAC CGAGCCGTTT GCCTGAAACG      60
GGCGCCGCGC CGGTACTGTT CGGACTTACC CCGCGCTCGT CGCGGCTBAC GTTGGCGSAG     120
ACCGGTAGCA CGCTGCTCTA CCGGCTGTTT AACCTGTGGG GTCCGCGCTT TCACGAGAGG     180
TATCCGAACG TCACCATCAC CGTTCAGGSC ACCGCTTCTG GTCCCGGGAT CCGCGAGGSC     240
GCGGCTGCGA CGGTCAACAT TCGGGCTTCC GACGCTTATC TGTCCGAAGG TGATATGGCC     300
GGGCACAAGG GGCTGATGAA GATCGCGGTA GGCATCTCCG CTCAGCAGGT CAACTACAAAC     360
CTGCGCGCGA TGAGCGAGCA CCTCAAGCTG AACGGAAAAA TCGTGGCGGC CATGTACCAG     420
GGACCCATCA AAAGCTGGGA CGACCCGCGA ATCGCTGCGC TCAACCCCGG CGTGAACCTG     480
CGCGCCACCG CGGTAGTTCC GGTGCACCCG TCGACCGGCT CGGCTGACAC CTTCCTTGTTC     540
ACCCAGTACC TGTCCAGCA AGATCCCGAG GCGCGGGGCA AGTCCCGCGG CTTCGCGCAG     600
ACCGTCCACT TCGCGCGGCT GCGGGGTGCG CTGGGTGAGA ACGGCAACGG CGGCATGGTG     660
ACCGCTTGCG CGGAGACACC GGGCTGCGTG GCTTATATCG GCATCAGCTT CCTCGACCAG     720
GCCAGTCNAC GGGGACTCGG CGAGGCCCAA CTAGGCAATA GCTCTGGCAA TTTCTTGTTC     780
CGCGACCGCC AAAGCATTCG GCGCGCGGCG GCTGGCTTCG CATCGAAAAC CCGCGCGAAC     840
CAGCGCATTT CGATGATCGA CCGGCGCGCG CCGGAACGCT ACCCGATCAT CAACTACGAG     900
TAGCCCATCG TCAACAACCG GCAAAAGGAC GCGCGCACCG CGCAGACCTT GCAGGCATTT     960
CTGCACTGGG CGATCACCGA CGGCAACGAG GCGCTGTTCC TCGACCAGGT TCATTTCCAG    1020
CGGCTGCGCG CCGCGGCTGT GAATTTGTCT GACGCTTTGA TCGCGACGAT TTCTTCGGA    1080
GCTGGCAGTG GGGAGGCTC AGGTGGAGCT TGTGGCGGGA GCGTGGCCAC AACGGCCGCG    1140
TGGCGCGGCT CGACCTCTCC AGTGGGACCG GCACTGGGGA CAGCTGTTGC CCGCGCACCA    1200
CGCGCGCGCG TCAACACCGC GATGCTCAG CCGCGCGATC CCAACCGCAG ACCTTCGCGC    1260
GCGGACCGGA AGGACCTGCG GCGACCTGTC ATTGCGGCAA ACCGACCGCA ACCTGTCGCG    1320
ATCGACAACC CGTTGCGAGG ATTGAGCTTC GCGCTGCGTG CTGGCTGGGT GAGTCTCGAC    1380
GCGCGCGACT TCGATACCGG TCGAGCACTC CTCAGCAAAA CCACCGGCGA CCGCGCATTT    1440
CGCGGACAGC CCGCGCGGCT GCGCAATGAC ACCGCTATCG TGCTCGGCGG GCTAGACCAA    1500
AAGCTTTTACG CGAGCGCGGA AGCCACCGAC TCCAAGGCGG CCGCGCGGTT GGGCTCGGAC    1560
ATGGGTAGCT TGTATAGCT CTACCGCGGC ACCCGATCA ACCAGGAAAC CGTCTCGGTC    1620
GACGCTAAGC GGGTGTCTCG AAGCGCGTCT TATTAGGAG TCGAGTTTCA GATCCGAGT    1680
AAGCTTAAGC GCGAGATCTG GACGGGCTTA ATCGGCTCGC CCGCGGCGAA CGCACCGGAC    1740
GCGCGCGCGC CTCAGGCTG GTTGTGCTA TGGCTCGGGA CCGCGAACAA CCGGTGGGAC    1800
AAGGGCGCGG CCAAGGCGCT GCGCGAATCG ATCGGCGCTT TGGTGGCGCG GCGCGCGGCG    1860
CGCGCACCGG CTCCTGCGAG GCGCGCTCGC GCGCGCGGCG CCGCGCGGGA AGTCTCTCTT    1920
ACCGCGACGA CACCGACACC GCAGCGGACC TTACCGGCTT GA

```

## (i) INFORMATION FOR SEQ ID NO:350:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Met Gly His His His His His His Gly Ser Lys Pro Pro Ser Gly Ser  
 1 5 10 15  
 Pro Gln Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser  
 20 25 30  
 Ser Pro Val Thr Leu Ala Gln Thr Gly Ser Thr Leu Leu Tyr Pro Leu  
 35 40 45  
 Phe Asn Leu Trp Gly Pro Ala Phe His Gln Arg Tyr Pro Asn Val Thr  
 50 55 60  
 Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala  
 65 70 75 80  
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Gln Gly  
 85 90 95  
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser  
 100 105 110  
 Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Gln His Leu Lys  
 115 120 125  
 Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr  
 130 135 140  
 Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro  
 145 150 155 160  
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr  
 165 170 175  
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Gln Gly Trp Gly  
 180 185 190  
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly  
 195 200 205  
 Ala Leu Gly Gln Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Gln  
 210 215 220  
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala  
 225 230 235 240  
 Ser Gln Arg Gly Leu Gly Gln Ala Gln Leu Gly Asn Ser Ser Gly Asn  
 245 250 255  
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe  
 260 265 270  
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro  
 275 280 285  
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Gln Tyr Ala Ile Val Asn  
 290 295 300  
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu  
 305 310 315 320  
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val  
 325 330 335  
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu  
 340 345 350  
 Ile Ala Thr Ile Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly  
 355 360 365  
 Gly Ser Gly Gly Ser Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr  
 370 375 380  
 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro  
 385 390 395 400  
 Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala  
 405 410 415  
 Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Val Ile Ala Pro  
 420 425 430



Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser  
 435 440 445  
 Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp  
 450 455 460  
 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro  
 465 470 475 480  
 Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg  
 485 490 495  
 Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala  
 500 505 510  
 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro  
 515 520 525  
 Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val  
 530 535 540  
 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys  
 545 550 555 560  
 Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn  
 565 570 575  
 Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly  
 580 585 590  
 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu  
 595 600 605  
 Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro  
 610 615 620  
 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr  
 625 630 635 640  
 Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala  
 645 650

# PATENT COOPERATION TREATY

## PCT

### DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a) and Rule 39)

Applicant's or agent's file reference 9532-023-228	<b>IMPORTANT DECLARATION</b>	Date of mailing (day/month/year) <b>22 JUNE 1999</b>
International application No. PCT/US99/03265	International filing date (day/month/year) 17 FEBRUARY 1999	(Earliest) Priority Date (day/month/year) 18 FEBRUARY 1998
International Patent Classification (IPC) or both national classification and IPC Please See Continuation Sheet.		
Applicant CORIXA CORPORATION		


This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
  - a. ☐ scientific theories.
  - b. ☐ mathematical theories.
  - c. ☐ plant varieties.
  - d. ☐ animal varieties.
  - e. ☐ essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
  - f. ☐ schemes, rules or methods of doing business.
  - g. ☐ schemes, rules or methods of performing purely mental acts.
  - h. ☐ schemes, rules or methods of playing games.
  - i. ☐ methods for treatment of the human body by surgery or therapy.
  - j. ☐ methods for treatment of the animal body by surgery or therapy.
  - k. ☐ diagnostic methods practiced on the human or animal body.
  - l. ☐ mere presentations of information.
  - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.
2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:
 

☐ the description
☐ the claims
☐ the drawings
3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the prescribed requirements prevents a meaningful search from being carried out:
 

☒ it does not comply with the prescribed standard  
☐ it is not in the prescribed machine readable form
4. Further comments:

Name and mailing address of the ISA/US  
Commissioner of Patents and Trademarks  
Box PCT  
Washington, D.C. 20231

Authorized officer  
  
MICHAEL WOODWARD

Facsimile No. (703) 305-3230

Telephone No. (703) 308-4028

Form PCT/ISA/203 (July 1992)\*

**DECLARATION OF NON-ESTABLISHMENT OF  
INTERNATIONAL SEARCH REPORT**

International application No.  
PCT/US99/03265

The International Patent Classification (IPC) or National Classification and IPC are as listed below:

IPC(S): A61K 38/00; C07K 1/00; C07K 16/00; C12Q 1/68; C12P 19/34; C07H 21/02, 21/04  
US Cl. 530/300, 350, 387.1; 435/6, 91.1, 91.2; 536/23.1, 24.3, 24.31, 24.32, 24.33